

FIGURE 1

CGGACGCGTGGGTGCGAGGCCAAGGTGACCGGGGACCGAGCATTTAGATCTGCTCGGTAGAC
 CCTGGTGCACCAACCACT**ATG**TTGGCTGCAAGGCTGGTGTGTCTCCGGACACTACCTTCTAGG
 GTTTTCCACCCAGCTTTTACCAAGGCTCCCTCTTGTGAAGAATTCCATCACGAAGAATCA
 ATGGCTGTTAACACCTAGCAGGGAATATGCCACCAAAACAAGAATTGGGATCCGGCGTGGGA
 GAAC TGCCCAAGAACTCAAAGAGGCAGCATTTGAACCATCGATGGAAAAAATATTTAAAT
 GATCAGATGGGAAGATGGTTTGTGCTGGAGGGGCTGCTGTTGGTCTTGGAGCATTGTGCTA
 CTATGGCTTGGGACTGTCTAATGAGATTGGAGCTATTGAAAAGGCTGTAATTTGGCCTCAGT
 ATGTCAAGGATAGAATTCTATCCACCTATATGTACTTAGCAGGGAGTATTGGTTTAACAGCT
 TTGTCTGCCATAGCAATCAGCAGAACGCCTGTTCTCATGAACTTCATGATGAGAGGCTCTTG
 GGTGACAATTGGTGTGACCTTTGCAGCCATGGTTGGAGCTGGAATGCTGGTACGATCAATAC
 CATATGACCAGAGCCCAGGCCCAAAGCATCTTGCTTGGTTGCTACATTCTGGTGTGATGGGT
 GCAGTGGTGGCTCCTCTGACAATATTAGGGGGTCTCTTCTCATCAGAGCTGCATGGTACAC
 AGCTGGCATTTGGGAGGGCTCTCCACTGTGGCCATGTGTGCGCCAGTGAAAAGTTTCTGA
 ACATGGGTGCACCCCTGGGAGTGGGCTGGGTCTCGTCTTTGTGTCTCATTTGGGATCTATG
 TTTCTTCCACCTACCACCGTGGCTGGTGCCACTTTTACTCAGTGGAATGTACGGTGGATT
 AGTTCTTTTTCAGCATGTTCTTCTGTATGATACCCAGAAAGTAATCAAGCGTGCAGAAGTAT
 CACCAATGTATGGAGTTCAAATAATGATCCCATTAAGTCTGATGCTGAGTATCTACATGGAT
 ACATTAATATATTTATGCGAGTTGCAACTATGCTGGCAACTGGAGGCAACAGAAAGAAAT**TC**
AGTGACTCAGCTTCTGGCTTCTGCTACATCAAAATCTTGTTTAATGGGGCAGATATGC
 ATTAAATAGTTTGTACAAGCAGCTTTCGTTGAAGTTTAGAAGATAAGAAACATGTCATCATA
 TTTAAATGTTCCGGTAATGTGATGCCTCAGGTCTGCCTTTTTTCTGGAGAATAAATGCAGT
 AATCCTCTCCCAATAAGCACACACATTTTCAATTCTCATGTTTGAGTGATTTTAAATGTT
 TTGGTGAATGTGAAACTAAAGTTTGTGTCATGAGAATGTAAGTCTTTTTTCTACTTTAAAA
 TTTAGTAGGTTCACTGAGTAACATAAAATTTAGCAAACTGTGTTTGATATTTTTTGGAGT
 GCAGAAATATTGAATTAATGTCATAAGTGATTTGGAGCTTTGGTAAAGGGACCAGAGAGAAG
 GAGTCACCTGCAGTCTTTTGTTTTTTAAATACTTAGAACTTAGCACTTGTGTATTGATTA
 GTGAGGAGCCAGTAAGAAACATCTGGGTATTTGGAAACAAGTGGTCATTGTTACATTCTTT
 GCTGAACCTTAACAAACTGTTTCATCTGAAACAGGCACAGGTGATGCATCTCCTGCTGTG
 CTTCTCAGTGCTCTCTTTCCAATATAGATGTGGTCATGTTTGACTTGTACAGAATGTTAATC
 ATACAGAGAATCCTTGATGGAATTATATATGTGTGTTTTACTTTTTGAATGTTACAAAAGGAA
 ATAACCTTTAAACTATTCTCAAGAGAAAATATTCAAAGCATGAAATATGTGCTTTTCCAG
 AATACAAACAGTATAGTCATG

FIGURE 2

MLAARLVCLRTLPSRVFHPAFTKASPVVKNSITKNQWLLTPSREYATKTRIGIRRGRTGQEL
 KEAALEPSMEKIFKIDQMGRWFFVAGGAAVGLGALCYYGGLSNEIGAIEKAVIWPQYVKDRI
 HSTYMYLAGSIGLTALSAIAISRTPVLMNFMMRGSWVTIGVTFAAMVGAGMLVRSIPYDQSP
 GPKHLAWLLHSGVMGAVVAPLTLGGPLLIRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPL
 GVGLGLVFVSSLGSMFLPPTTVAGATLYSVAMYGGVLVFSMFLLYDTQKVIKRAEVSPMYGV
 QKYDPINSMLSIYMDTLNIFMRVATMLATGGNRKK

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FIGURE 3

GAAGGCTGCCTCGCTGGTCCGAATTCCGGTGGCGCCACGTCGCGCCGCTTCCGCGCTTCTGCAT
 CGCGGCTTCGGCGGCTTCCACCTAGACACCTAACAGTCGCGGAGCCGGCCGCGCTCGTGAGGG
 GGTCCGACGCGGGAGTCGGGGGCTTGTGCATCTTGGCTACCTGTGGGTGCGAAGATGTCGCG
 ACATCGGAGACTGGTTCAGGAGCATCCCGCGCATCAGCGCGTATTGGTTCCGCGCCACCGCTC
 CGCGTCCCTTGGTCGGCAAACTCGGCTCATCAGCCCGGCTACCTCTTCCCTCGGCGCGCA
 AGCCTTCCTTTTCTCGCTTTCAGATTGGAGGCCAATCACTGCCACCTTTATTTCCCTGTGG
 GTCCAGGAACCTGATTTCTTTATTTGGTCAATTTATATTTCTTATACAGTATTTACGCGCA
 CTTGAAACAGGAGCTTTTGATGGGAGGCCAGCAGACTATTTATTCATGCTCCTCTTTAACTG
 GATTTGCATCGTGATTACTGGCTTAGCAATGGATATGCAGTTGCTGATGATTTCTCTGATCA
 TGTCAGTACTTTATGCTGGGCCAGCTGAACAGAGACATGATTGATCATTTTGGTTTGGGA
 ACACGATTTAAGGCTGCTATTTACCTGGGTTATCCTTGGATTCAACTATATCATCGGAGG
 CTCGGTAATCAATGAGCTTATTTGGAATCTGGTGGACATCTTTATTTTTCTTAATGTTCA
 GATACCCAATGGACTTGGGAGGAAGAAATTTTCTATCCACACCTCAGTTTTTGTACCGCTGG
 CTGCCAGTAGGAGAGGAGGAGTATCAGGATTTGGTGTGCCCCCTGCTAGCATGAGGCGAGC
 TGCTGATCAGAATGGCGAGGCGGAGACACAACCTGGGCGCAGGGCTTTCGACTTGGAGACC
 AGTGAAGGGGCGGCTCGGGCAGCGCTCCTCTCAAGCCACATTTCTCCAGTGCTGGGTG
 CACTTAACAACCTGCTTCTGGCTAACACTGTTGGACCTGACCCACACTGAATGTAGTCTTTC
 AGTACGAGACAAAGTTTCTTAAATCCCGAAGAAAATATAAGTGTTCCACAAAGTTTACAGAT
 TCTCATTTCAAGTCTCTACTGCTGTGAAGAACAAATACCAACTGTGCAAAATGCAAACTGAC
 TACATTTTTTGGTGTCTTCTCTTCTCCCTTTCCGCTCGAATAATGGGTTTTAGCGGGTCTCT
 AATCTGCTGGCATGTAGCTGGGCTGGGTACCAAACCCCTTCCAAAGGACCTTATCTCTT
 TCTTGACACATGCGCTCTCTCCACCTTTTCCCAACCCCCACATTTGCAACTAGAAAAGTTG
 CCCATAAAATTTGCTCTGCTCTTGACAGGTTCTGTTATTTATTGACTTTTGCCAAAGGCTGGTC
 ACAACAAATCATATTACAGTTATTTTCCCTTTTGGTGGCAGAACTGTTACCAATAGGGGGAG
 AAGACAGCCACGGATGAAGCTTTCTCAGCTTTTGGAAATGCTTCGACTGACATCCGTTGTT
 AACCGTTTGGCACTCTCAGATATTTTTATAAAAAAAGTACCACGTAGTTCATGAGGGCCA
 CAGATTTGGTTATTAATGAGATACGAGGGTTGGTGTCTGGGTGTTTGTCTGAGCTAAGTGA
 TCAAGACTGTAGTGGATTTGACGTAAACATGGGTTAGGTTTAAACCATGGGGGATGACCCCT
 TTTGCGTTTCATATGTAGCCCTACTGGCTTTGTGTAGCTGGAGTAGTTGGGTTGCTTTGTGT
 TAGGAGGATCCAGATCATGTTGGCTACAGGGAGATGCTCTCTTTGAGAGGTCTGGGCATGT
 ATTCCCATTTCAATCTCATCTCGGATATGTGTTCAATTGAGTAAAGGAGGAGACCCCTCATA
 CGCTATTTAAATGTCACTTTTTGGCTATCCCCGTTTTTGGTCAATGTTCAATTAATGT
 GAGGAAGGCGCAGCTCCTCTGTCACGTAGATCATTTTTTAAAGCTAATGTAAGCACATCTA
 AGGGAATAACATGATTTAAGGTTGAAATGGCTTTAGAATCATTTGGGTTTGAGGGGTGTGTTA
 TTTTGAGTCATGAATGTACAAGCTCTGTGAATCAGACCAGCTTAAATACCCACACTTTTTT
 TCGTAGGTGGGCTTTTCTATCAGAGCTTGGCTCATAACCAAAATAAGTTTTTGAAGGCCA
 TGGCTTTTACACAGTTATTTTATTTATGACGTTATCTGAAAGCAGACTGTTAGGAGCAGT
 ATTGAGTGGCTGTACACTTTTGGGCAACTAAAAGGCTTCAAACGTTTTGATCAGTTTCTT
 TTCAGGAACATTGTGCTCTAACAGTATGACTATCTTTCCCCCACTTAAACAGTGTGAT
 GTGTGTTATCTAGGAAATGAGAGTTGGCAAACAACTTCTCATTTTGAATAGAGTTTGTGTG
 TACTTCTCATATTTAATTTATATGATAAAATAGGTGGGAGAGTCTGAACCTTAACTGTCA
 TGTTTTGGTGTTCATCTGTGGCCCAATAAAGTTTACTTGAATAATTTAGAGGCCATTACT
 CCAATTAAGTTGCACGTACACTATTGTACAGGCTGGAGACTCATTTGATGTATAAGAATA
 TTTCTGACAGTGAGTGACCCGAGTCTGGTGTACCTCTTACAGTCAAGTGTGCTGCGAG
 CAGTCATTTTTTCTAAAGTTTACAAGTATTTAGAATTTTTCAGTTCAGGGCAAAATGTTT
 ATGAAGTTATCTCTTTAAACATGGTTAGGAAGCTGATGAGCTTATGATTTTGTCTGGATT
 ATGTTTCTGGAATAATTTTACCAAACAAGCTATTTGAGTTTGTACTGACAAGGCAAAACA
 TGACAGTGGATTCTCTTTACAAATGGAATAAAAAATCCTTTATTTGTATAAAGGACTTCCC
 TTTTGTAACTAATCCTTTTTATTGGTAAAAATGTAAATTAATATGTCACACTTG

FIGURE 4

MSDIGDWFRSIPAITRYWFAATVAVPLVGKLG LISPAYLFLWPEAFLYRFQIWRPITATFYF
PVGPGTGFLYLVLNLYFLYQYSTRLETGAFDGRPADYLFMLLFNWICIVITGLAMDMQLLMIP
LIMSVLYVWAQLNRDMIVSFWFGTRFKACYLPWVILGFNYIIGGSVINELIGNLVGHLYFFL
MFRYPMDLGGRNFLSTPQFLYRWLPSRRGGVSGFGVPPASMRRAADQNGGGGRHNWGQGFRLL
GDQ

Transmembrane domain:

amino acids 98-116, 152-172

N-myristoylation site.

amino acids 89-95, 168-174, 176-182, 215-221, 221-227, 237-243

Glycosaminoglycan attachment site.

amino acids 218-222

FIGURE 5

GGGGCCCGCGGTCTAGGGCGGCTACGTGTGTTGCCATAGCGACCATTTTGCATTAACTGGTTG
 GTAGCTTCTATCCTGGGGGCTGAGCGACTGCGGGCCAGCTTTCCCCTACTCCCTCTCGGCT
 CCTTGTGGCCCAAAGGCTTAACCGGGGTCGCGGGTCTGGCTAGGGATCTTCCCCGTGCG
 CCTTTGGGCGGGATGGCTGCGGAAGAAGAAGACGAGGTGGAGTGGGTAGTGGAGAGCATCG
 CGGGGTTCCTGCGAGGGCCAGACTGGTCCATCCCCATCTTGGACTTTGTGGAACAGAAATGT
 GAAGTTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCCAGAGCCGGTGATTTTGGT
 GGCCTGTGTTCCCCTTGTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATTC
 ATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAATT
 AATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAGGC
 CATTTTGCAACCTGTGTTGGCAGCAGAAGATTTACTATCTTTAAAGCAATGATGGTCCAGA
 AAAACATTGAAATGCAGCTGCAAGCCATTGCAATAATTCAAGAGAGAAATGGTGTATTACCT
 GACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAAATCCT
 GAGGGAAGTCTTAGAAAAATCAAAGAGGAATATGACCAGGAAGAAGAAAGGAAGAGGAAAA
 AACAGTTATCAGAGGCTAAAAACAGAAGAGCCACAGTGCACTTCCAGTGAAGCTGCAATAATG
 AATAATTCCCAAGGGGATGGTGAACATTTTGCACACCCACCTCAGAAGTTAAATGCATTT
 TGCTAATCAGTCAATAGAACCTTTGGGAAGAAAAGTGGAAAGGTCTGAAACTTCCTCCCTCC
 CACAAAAAGGCCTGAAGATTCCTGGCTTAGAGCATGCGAGCATTGAAGGACCAATAGCAAAC
 TTATCAGTACTTTGGAACAGAAGAAGCTTCGGCAACGAGAACACTATCTCAAGCAGAAGAGAGA
 TAAGTTGATGTCCATGAGAAAGGATATGAGGACTAAACAGATACAAAATATGGAGCAGAAAG
 GAAAACCCACTGGGGAGGTAGAGGAAATGACAGAGAAACCAGAAATGACAGCAGAGGAGAAG
 CAAACATTACTAAAGAGGAGATTGCTTGCAGAGAAACTCAAAGAAGAAGTTATTAATAAGTA
ATAATTAAGAACAATTTAACAAAATGGAAGTTCAAATTGTCTTAAAAATAAATTATTTAGTC
 CTTACACTG

FIGURE 6

MAAEEEEDEVWVESIAGFLRGPDWSIPILDFVEQKCEVNCKGGHVITPGSPPEPVILVACVP
LVFDDEEESKLTYTEIHQEYKELVEKLLEGYLKEIGINEDQFQEACTSPLAKTHTSQAILQP
VLAAEDFTIFKAMMVQKNIEMLQAIRIIQERNGLPDCLTDGSDVVSLEHEEMKILREVL
RKSKEEYDQEEERKRKKQLSEAKTEEPTVHSSEAAIMNNSQGDEGHFAHPPSEVKMHFANQS
IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPIANLSVLGTEELRQREHYLKQKRDKLMS
MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAEEKQTLLKRLLAEKLKEEVINK

N-glycosylation sites.

amino acids 224-228, 246-250, 285-289

N-myristoylation site.

amino acids 273-279

Amidation site.

amino acids 252-256

Cytosolic fatty-acid binding proteins.

amino acids 78-108

FIGURE 7

GGGCACAGCACATGTGAAGTTTTTGTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGAT
TCATCAGGAATACAAAGAAGCTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAA
TTAATGAAGATCAATTTCAAGAAGCATGCACCTTCTCCTCTTGCAAAGACCCATACATCACAG
GCCATTTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCC
AGAAAAACATTGAAATGCAGCTGCAAGCCATTGGAATAATTCAAGAGAGAAATGGTGTATTA
CCTGACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAT
CCTGAGGGAAGTTCTTAGAAAATCAAAGAGGAATATGACCAGGAA



FIGURE 8

GCGTGGTTTTTGTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTTGCGCTATACCTACTG
 TAGCTTCTCCACGTATGGACCTTAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTG
 TCTCAGCTCTAGGATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTAACAAAC
 AGTGGAAATGGGAAAAACAGTGTCTGAGTCATCCTGTAATATGCTCCTTGTCAACAATGTATAC
 ATTCCTGCTAGGTGCCATATTCATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATT
 CTGCCAATGAAGAAAAAAGTATGATTATCTTCCAACACTGTGAATGTGTCTCAGAAGCTG
 GTGAAGCTAGTTTTCTGTGTGCTTGTGTCATTCTGTGTTATAAAGAAAAGATCATCAAAGTAG
 AAATTTGAAGATATGCTTCTCGGAAGGAATTTCTGATTTTCATGAAGTGGTCCATTCTCGCCT
 TTCTTTATTCTCGGATAACTTGATTGCTCTTCTATGTCCGTGCTATCTTCAACCCGATG
 GCTGTTTATCTTCAAAATTTTAGCATTATAACAACAGCTCTTCTATTAGGATAGTGTGAA
 GAGGCGCTAAACTGGATCCAGTGGGCTTCCCTCCTGACTTATTTTTGTCTATTGTGGCCT
 TGACTGCCGGGACTAAAACCTTACAGCACAACTTGGCAGGACGTGGATTTCATCAGATGCC
 TTTTTCAGCCCTTCCAATTCCTGCCTTCTTTTCAGAAGTGAGTGTCCAGAAAAGACAATTG
 TACAGCAAGGAATGGACTTTTCTGAAGCTAAATGGAACACCACAGCCAGAGTTTTCAGTC
 ACATCCGCTCTTGGCATGGGCCATGTCTTATTATAGTCCAGTGTTTTATTCTTCAATGGCT
 AATATCTATAATGAAAGATACTGAAAGGAGGGGAACAGCTCACTGAAGCATCTTCATACA
 GAACAGCAAACTCTATTCTTTGGCATTCTGTTAATGGGCTGACTCTGGGCCCTCAGAGGA
 GTAACCGTGATCAGATTAGAAGCTGTGGATTTTTTTATGGCCACAGTGCATTTTCAGTAGCC
 CTTATTTTGTAACTGCATTTCCAGGGCCTTTCAGTGGCTTTCATTCTGAAGTTCCTGGATAA
 CATGTTCCATGTCTTGATGGCCAGGTTACCAGTGTCAATTACAGCAAGTGTCTGTCTCTGG
 TCTTTGACTTCAGGCCCTCCCTGGAATTTTTCTTGAAGCCCCATCAGTCCTTCTCTCTATA
 TTTATTTATAATGCCAGCAAGCCTCAAGTTCGGAATACGCACCTAGGCAAGAAAGGATCCG
 AGATCTAAGTGGCAATCTTTGGGAGCGTCCAGTGGGGATGGAGAAGAACTAGAAAGACTTA
 CCAAAACCAAGAGTGATGAGTCAGATGAAGATACTTTCTAACTGGTACCCACATAGTTTGCA
 GCTCTTTGAACCTTATTTTCAATTTTCAGTGTGTTGTAATATTATCTTTTTCACITTTGATA
 AACCAGAAATGTTTCTAAATCCTAATATCTTTGCATATATCTAGCTACTCCCTAAATGGTT
 CCATCCAAGGCTTAGAGTACCCAAAGGCTAAGAAATCTTAAAGAACTGATACAGGAGTAACA
 ATATGAAGAATTCATTAATATCTCAGTACTTGATAAATCAGAAAGTTATATGTGCAGATTAT
 TTTCTTGGCCTTCAAGCTTCCAAAAAAGCTGTAATAATCATGTTAGCTTATAGCTTGTATAT
 ACACATAGAGATCAATTTGCCAAATATTCACAATCATGTAGTCTTAGTATTACATGCCAAAGT
 CTTCCCTTTTAAACATTATAAAAGCTAGGTTGTCTCTTGTAAATTTAGGGCCCTAGAGTAGT
 CATTTTGCAGTAAAGAGCAACGGGACCTTTCTAAAAACGTTGGTTGAAGGACCTAAATAC
 CTGGCCATACCATAGTACTTTGGGATGATGTAGTCTGTGCTAAATATTTTGTGAAGAGCAGT
 TTCTCAGACACAACATCTCAGAATTTAATTTTTAGAAATTCATGGGAAATTGGATTTTTGT
 AATAATCTTTTGATGTTTTAAACATTGGTTCCCTAGTCACCATAGTTACCAGTGTGATTTTTA
 AGTCATTTAAACAGCCACGGTGGGCTTTTTCTCCTCAGTTTGAAGAGAGAAAAATCTGAT
 GTCATTACTCCTGAATTTATACATTTTGAGAGAATAAGAGGGCACTTTTATTTTATAGTTACT
 AATCAAGCTGTGACTATTGTATATCTTTCCAAGAGTTGAATGCTGGCTCAGATCATAC
 CAGATTGTGAGTGAAGCTGATGCCTAGGAACCTTTAAAGGGATCCTTTCAAAGGATCACTT
 AGCAACACATGTTGACTTTTAACTGATGATGAATATTAATCTCTAAAAATAGAAAGACC
 AGTAATATATAAGTCACTTTTACAGTGCTACTTCACTTAAAGTGCATGGTATTTTTCATG
 GTATTTTGCATGCAGCCAGTTAACTCTCGTAGATAGAGAAGTCAGGTGATAGATGATATTA
 AAATTAGCAAAACAAAGTGACTTGCTCAGGCTCATGCAGCTGGGTGATGATAGAAGAGTGGG
 CTTTAACTGCAGGCCCTGTATGTTTACAGACTACCATACTGTAAGATGAGCTTTATGGTGT
 CATTTCTCAGAACTTATACATTTCTGCTCTCCTTTCTCCTAAGTTTCATGCAGATGAATATA
 AGGTAATATACATTATATAATTCATTTGTGATATCCACAATAATGACTGGCAAGAAATTG
 GTGGAATTTGTAATTAATAATTTATTAACCT

FIGURE 9

MEKQCCSHPVICSLSTMYTFLGAI FIALSSSRILLVKYSANEENKYDYLPTTVNVCSELVK
 LVFCVLVSFCVIKKDHQSRNLKYASWKEFSDFMKWSIPAFLYFLDNLIVFYVLSYLQPAMAV
 IFSNFSIIPTALLFRIVLKRRLNWIQWASLLTLFLSIVALTAGTKTLQHNLAGRGRGHDAFF
 SPSNSCLLFRSECPKRDNCTAKEWTFPEAKWNNTARVFSHIRLGMGHVLIIVQCFISSMANI
 YNEKILKEGNQLTESIFIQNSKLYFFGILFNGLTLGLQRSNRDQIKNCGFFYGHSFAFSVALI
 FVTAFQGLSVAFILKFLDNMFHVLMAQVTTVIITTVSVLVDFRPSLEFFLEAPSVLISIFI
 YNASKPQVPEYAPRQERIRDL SGNLWERSSSGDGEELERLTKPKSDEDEDTF

Transmembrane domains:

amino acids 16-36 (type II), 50-74, 147-168, 229-250, 271-293,
 298-318, 328-368

N-glycosylation sites.

amino acids 128-132, 204-208, 218-222, 374-378

Glycosaminoglycan attachment site.

amino acids 402-406

N-myristoylation sites.

amino acids 257-263, 275-281, 280-286, 284-290, 317-323

FIGURE 10

CGTGCCTGCGCAATGGGTGTCGGGTCCGCTTTTTCCCAATCCGGACGTAATCGTGGTTTTTG
TTCTGCAATAGGCGGCTTAGAGGGAGGGGCTTTTCGCCCTATACCTACTGTAGCTTCTCCAC
GTATGGACCCTAAAGGCTACTGCTGCTACTACGGGGCTAGACAGTTACTGTCTCAGCTCTAG
GATGTGCGTTCTTCCACTAGAAGCTCTTCTGAGGGAGGTAATTAaaaaaCAGTGGAATGGAA
AAACAGTGTCTGTAGTCATCCTGTAATATGCTCCTTGTCACAATGTATACATTCTGCTAGG
TGCCATATTCAATTGCTTTAAGCTCAAGTCGCATCTTACTAGTGAAGTATTCTGCCAATGAAG
AAAACAAGTATGATTATCTTCCAACACTGTGAATGTGTGCTCAGAACTGGTGAAGCTAGTT
TTCTGTGTGCTTGTGTCAATTCTGTGTTATAAAGAAAGATCATCAAAGTAGAAATTTGAAATA
TGCTTCCTGGAAGGAATTCTCTGATTTTCATGAAGTGGTCCATTCTGCCTTTCTTTATTTCC
TGGATAACTTGATTGTCTTCTATGTCCTGTCCATCTTCAACCAGCCATGGCTGTTATCTTC
TCAAATTTTAGCATTATAACAACAGCTCTTCTATTAGGATAGTGTGAAGAGGCGCTCTAAA
CTGGATCCAGTGGGCTTCCCTCCTGACTTTATTTTTGTCTATTGTGGCCTTGACTGCCGGGA
CTAAAACTTTA

FIGURE 11

CGGACGCGTGGGCGGACGCGTGGGCGGACGCGTGGGCGGGCTTGGCTAGCGCGCGGCGGCC
GTGGCTAAGGCTGCTACGAAGCGAGCTTGGGAGGAGCAGCGGCTGCGGGGACAGAGGACAT
CCCCTCTACCAAGTCCCAAGCGGCGTGGCCCGCGGGTTCATGGCCAAAGGAGAAGGCGCCGAG
AGCGGCTCCGCGGCGGGCTGCTACCCACAGCATCCTCCAAAGCACTGAACGCCCGGCCCA
GGTGAAGAAAGAACCGAAAAAGAAACAACAGTTGCTCTGTTTGAACAAGCTTTGCTATG
CACTTGGGGGAGCCCCCTACCAGGTGACGGGCTGTGCCCTGGGTTTCTTCCTTCAGATCTAC
CTATTGGATGGCTCAGGTGGGCCCTTCTCTGCCCTCCATCATCCTGTTTGTGGGCCGAGC
CTGGGATGCCATCACAGACCCCTGGTGGGCTCTGCATCAGCAAATCCCCCTGGACCTGCC
TGGGTGCGCTTATGCCCTGGATCATCTTCTCCACGCCCTGGCCGTATTGCCTACTTCCCTC
ATCTGGTTCTGTGCCGACTTCCCACAGGCCAGACCTATTGGTACCTGCTTTTCTATTGCCT
CTTTGAAACAATGGTCACGTGTTCCATGTTCCCTACTCGGCTCTCACCATGTTTCATCAGCA
ACCGAGCAGACTGAGCGGGATTCTGCCACCGCCTATCGGATGACTGTGGAAGTGTGGGCAC
AGTGTGGGCACGGCGATCCAGGGACAAATCGTGGGCCAAGCAGACACGCCTTGTTTCCAGG
ACTTCAATAGCTCTACAGTAGCTTCAAAAGTGCCAACCATACACATGGCACCACCTTCACAC
AGGGAACAGCAAAAGGCATACCTGCTGGCAGCGGGGTCATTGTCTGTATCTATATAATCTG
TGCTGTCTCCTGATCCTGGGCGTGCGGGAGCAGAGAGAACCCTATGAAGCCAGCAGTCTG
AGCCAATCGCTACTTCCGGGCTTACGGCTGGTCTGAGGCCACGGCCCATACATCAAACTT
ATTACTGGCTTCTCTTCACTCCTTGGCTTTCATGCTGGTGGAGGGAACTTTGTCTTGT
TTGCACCTACACCTTGGGCTTCCGCAATGAATCCAGAATCTACTCCTGGCCATCATGCTCT
CGGCCACTTTAACCATTCCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCT
GTATATGTTGGGATCTCATCAGCAGTGCCATTCTCATCTTGGTGGCCCTCATGGAGAGTAA
CCTCATCATTACATATGGGCTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCCTTCTTAC
TACCCTGGTCCATGCTGCCGTATGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCAT
GGAACCGAGCCCCTCTTCTTCTCCTTCTATGTCTTCTTACCACAGTTTGCCTCTGGAGTGT
ACTGGGCATTCTACCCCTCAGTCTGGACTTGTGAGGGTACCAGACCCGTGGCTGCTCGCAGC
CGGAACGTGTCAAGTTTACACTGAACATGCTCGTGACCATGGCTCCCATAGTTCTCATCTCTG
CTGGGCTGTGCTCTTCAAAATGTACCCCATTTGATGAGGAGAGGCGGGCGCAGAATAAGAA
GGCCCTGCAGGCACTGAGGGACGAGGCCAGCAGCTCTGGCTGCTCAGAAACAGACTCCACAG
AGCTGGCTAGCATCCTCTAGGGCCCGCCACGTTGCCCGAAGCCACCATGCAGAAAGGCCACAG
AAGGGATCAGGACCTGTCTGCCGGCTTGTGAGCAGCTGGACTGCAGGTGCTAGGAAGGGAA
CTGAAGACTCAAGGAGGTGGCCACAGCACTTGCTGTGCTCACTGTGGGCCGGCTGCTCTG
TGGCCTCCTGCCTCCCCTCTGCCTGCCTGTGGGGCCAAAGCCCTGGGGCTGCCACTGTGAATA
TGCCAAAGACTGATCGGGCTAGCCGGAACACTAATGTAGAAACCTTTTTTTTACAGAGCC
TAATTAATACTTAATGACTGTGTACATAGCAATGTGTGTATGTATATGCTGTGAGCTA
TTAATGTTATTATTTTCATAAAAGCTGGAAAGC

MWLRWALS L P F S S C L W A E F G M P S Q T P W W A S A N P F G P A W A L C P G S S S P R F W P S L T S S S G
S C P T S H T A R P I G T C F S I A S L K Q W S R V S M F P T R L S P C S S A T E Q T E R D S A T A Y R M T E V L G T V L
G T A I Q G Q I V G Q A D T P C F Q D F N S S T V S A Q S A N H T H G T T S H R E T Q K A Y L L A A G V I V C I Y I I C A V
I L I L G V R E Q R E P Y E A Q Q S E P I A Y F R G L R L V M S H G P Y I K L I T G F L F T S L A F M L V E G N F V L F C T
Y T L G F R N E F Q N L L A I M L S A T L T I P I Q W F L T R F G K K T A V Y V G I S S A V P F L I L V A L M E S N L I
I T Y A V A V A A G I S V A A F L L P W S M L P D V I D D F H L K Q P H F H G T E P I F F S F Y V F T K F A S G V S L G
I T S L S L D F A G Y Q T R C S Q P E R V K F T L N M L V T M A P I V L I L L G L L L F K M Y P I D E R R R Q N K K A L
Q A L R D E A S S G C S E T D S T E L A S I L

FIGURE 13

GGGAAACGAAAAGGCATACCTGCTGGCAGCGGGGGTCATTGTCTGTATCTATATAATCTGT
GCTGTCATCCTGATCCTGGGCGTGC GGGAGCAGAGAGAACCCTATGAAGCCCAGCAGTCTGA
GCCAATCGCCTACTTCCGGGGCCTACGGCTGGTCATGAGCCACGGCCCATACATCAAACCTTA
TTACTGGCTTCCTCTTCACCTCCTTGGCTTTTCATGCTGGTGGAGGGGAACTTTGTCTTGTTT
TGCACCTACACCTTGGGCTTCCGCAATGAATTCCAGAATCTACTCCTGGCCATCATGCTCTC
GGCCACTTTAACCATTCCCATCTGGCAGTGGTTCTTGACCCGGTTTGGCAAGAAGACAGCTG
TATATGTTGGGATCTCATCAGCAGTGCCATTTCTCATCTTGGTGGCCCTCATGGAGAGTAAC
CTCATCATTACATATGCGGTAGCTGTGGCAGCTGGCATCAGTGTGGCAGCTGCCTTCTTACT
ACCCCTGGTCCATGCTGCCTGATGTCATTGACGACTTCCATCTGAAGCAGCCCCACTTCCATG
GAACCGAGCCCAT

FIGURE 14

GGGGCTTCGGCGCCAGCGCCAGCGCTAGTCGGTCTGGTAAGGATTTACAAAAGGTGCAGGT
 ATGAGCAGGTCTGAAGACTAACATTTTGTGAAGTTGTAAAACAGAAAACCTGTTAGAAATGT
 GGTGGTTTCAGCAAGGCTCAGTTTCCTTCCTTCAGCCCTGTAAATTTGGACATCTGCTGCT
 TTCATATTTTCATACATTACTGCAGTAACACTCCACCATATAGACCCGGCTTTACCTTATAT
 CAGTGACACTGGTACAGTAGCTCCAGAAAAATGCTTATTTGGGGCAATGCTAAATATTGCGG
 CAGTTTTATGCATTGCTACCATTTATGTTTCGTTATAAGCAAGTTCATGCTCTGAGTCCTGAA
 GAGAACGTTATCATCAAATTAACAAGGCTGGCCTTGACTTGAATACTGAGTTGTTTAGG
 ACTTTCATTTGTGGCAAACCTCCAGAAAAACAACCTTTTTGCTGCACATGTAAGTGGAGCTG
 TGCTTACCTTTGGTATGGGCTCATTATATATGTTTGTTCAGACCATCCTTTCTACCAAATG
 CAGCCCAAATCCATGGCAAACAAGTCTTCTGGATCAGACTGTTGTGGTTATCTGGTGTGG
 AGTAAGTGCACCTTAGCATGCTGACTTGCTCATCAGTTTGCACAGTGGCAATTTGGGACTG
 ATTTAGAACAGAACTCCATTGGAACCCCGAGGACAAAGGTTATGTGCTTCACATGATCACT
 ACTGCAGCAGAATGGTCTATGTCATTTTCCTTCTTTGGTTTTTTCCTGACTTACATTCTGTA
 TTTTCAGAAAATTTCTTTACGGGTGGAAGCCAATTACATGGATTAACCTCTATGACACTG
 CACCTTGCCCTATTAACAATGAACGAACACGGCTACTTTCAGAGATATTGATGAAAGGAT
 AAAATATTTCTGTAATGATTATGATTCTCAGGGATTGGGGAAAGGTTACAGAAAGTTGCTTA
 TTCTTCTCTGAAATTTCAACCACCTTAATCAAGGCTGACAGTAACACTGATGAATGCTGATA
 ATCAGGAAACATGAAAGAAGCCATTTGATAGATTATTCTAAAGGATATCATCAAGAAGACTA
 TTA AAAACACCTATGCCTATACTTTTTTATCTCAGAAAAATAAGTCAAAAGACTATG

MWWFQQLGSLFLPSALVIWTSAAFIIFS YITAVTLHHIDPALPYISDTGTVAPEKCLFGAMLNI
 AAVLCIATIYVRYKQVHALSPEENV I I KLNKAGLVGLGLSCLGLSIVANFQKTTLFAAHVSG
 AVLTFPGMGSGLMYFVQTILSYQM QPKIHGKQVFWIRLLLVICVGSALSMLTCSVLHSGNF
 TDLEQKLHWNPEDKGYVLHMITTA EAWSMSFSFFGFFLT YIRDFQSLRLVEANLHGLTLYD
 TAPCPINNERTLLSRDI

FIGURE 16

CGGACGCTTGGGCNCGCCAGCGGCCAGCGCTAGTCGGTCTGGTAAGTGCCTGATGCCGAGT
TCCGTCTCTCGGGTCTTTTCCTGGTCCCAGGCAAAGCGGAGCGGAGATCCTCAAACGGCCTA
GTGCTTCGCGCTTCCGGAGAAAATCAGCGGTCTAATTAATTCCTCTGGTTTGTGAAGCAGT
TACCAAGAATCTTCAACCCCTTCCCACAAAAGCTAATTGAGTACACGTTCCCTGTTGAGTACA
CGTTCCTGTTGATTTACAAAAGGTGCAGGTATGAGCAGGTCTGAAGACTAACATTTTGTGAA
GTTGTAAAACAGAAAACCTGTTAGAAATGTGGTGGTTTCAGCAAGGCCTCAGTTTCCTTCCT
TCAGCCCTTGTAATTTGGACATCTGCTGCTTTCATATTTTCATACATTACTGCAGTAACACT
CCACCATATAGACCCGGCTTTACCTTATATCAGTGACACTGGTACAGTANC

FIGURE 17

CCCACGCGTCCGCCCCCGCTGCGTCCCGAGTGCAAGTGAGCTTCTCGGCTGCCCCGCGGG
 CCGGGGTGCGGAGCCGACATGCGCCCCGCTTCTCGGCCTCCTTCTGGTCTTCGCCGGCTGCAC
 CTTGCGCTTGTACTTGCTGTGACGCGACTGCCCCGCGGCGGAGACTGGGCTCCACCGAGG
 AGGCTGGAGGCAGGTGCGTGTGGTTCCCTCCGACCTGGCAGAGCTGCGGGAGCTCTCTGAG
 GTCTTTCGAGAGTACCGGAAGGAGCACCAGGCCTACGTGTTCTGCTCTTCTGCGGCGCCTA
 CCTCTACAAACAGGGCTTTGCCATCCCCGGCTCCAGCTTCTCTGAATGTTTTAGCTGGTGCCT
 TGTTTGGGCCATGGCTGGGGCTTCTGCTGTGCTGTGTGTTGACCTCGGTGGGTGCCACATGC
 TGCTACCTGCTCTCCAGTATTTTTGGCAAACAGTTGGTGGTGTCTACTTTCTGTATAAAGT
 GGCCCTGCTGCAGAGAAAGGTGGAGGAGAACAGAAACAGCTTGTTTTTTTCTTATGTTTT
 TGAGACTTTTCCCATGACACCAAAGTGGTCTTGAACCTCTCGGCCCCAATCTGAACATT
 CCCATCGTGCAGTTCTTCTTCTCAGTTCTTATCGGTTTGATCCCATATAAATTCATCTGTGT
 GCAGACAGGTCATCTGTCAACCTAACCTCTCTGGATGCTCTTTTCTCTGGGACACTG
 TCTTTAAGCTGTTGGCCATTGCCATGGTGGCATTAAATCTGGAACCCCTATTAAAAAATTT
 AGTCAGAAACATCTGCAATTGAATGAAACAAGTACTGCTAATCATATACACAGTAGAAAAGA
 CACATGACTCTGGATTTTCTGTTTGGCCATCCCTGGACTCAGTTGCTTATTTGTGTAATGGA
 TGTGGTCTCTAAAGCCCCCTATTGTTTTGATTGCCTTCTATAGGTGATGTGGACACTGTG
 CATCAATGTGCAGTGTCTTTTCAGAAAGGACACTCTGCTCTTGAAGGTGATTACATCAGGT
 TTTCAAACCAGCCCTGGTGTAGCAGACACTGCAACAGATGCCTCCTAGAAAAATGCTGTTTGT
 GGCCGGGCGCGGTGGCTCAGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCCGGTGATTCT
 ACAAGGTGAGGAGTTCAAGACCAGCCTGGCCAAGATGGTGAATCCTGTCTCTAATAAAAAAT
 ACAAAAAATTAGCCAGGCGTGGTGGCAGGCACCTGTAATCCAGCTACTCGGGAGGCTGAGGC
 AGGAGAAATTGCTTGAACCAAGGTGGCAGAGGTTGCAGTAAGCCAAGATCACACCCTGCACT
 CCAGCCTGGGTGATAGAGTGAGACACTGTCTTGAC

FIGURE 18

MRPLLGLLLVFAGCTFALYLLSTRLPGRRLGSTEAGGRSLWFPSDLAELRELSVLREYR
 KEHQAYVFLLFCGAYLYKQGFAIPGSSFLNLVLAGALFGPWLGLLLCCVLTSVGATCCYLLSS
 IFGKQLVVSYPDPKVALLRKVEENRNSLFFFLFLRLFPMPNWFNLNSAPILNIPVQFF
 FSVLI GLIPYNFICVQTGSILSTLTSLDALFSWDTVFKL LAIAMVALIPGT LIKKFSQKHLQ
 LNETSTANHIHSRKDT

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domains:

amino acids 101-123, 189-211

N-glycosylation sites.

amino acids 172-176, 250-254

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 240-244, 261-265

N-myristoylation site.

amino acids 13-19, 104-110, 115-121, 204-210

Amidation site.

amino acids 27-31

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 4-15

Protein splicing proteins.

amino acids 25-31

Sugar transport proteins.

amino acids 162-172

FIGURE 19

CCGAGGCGGGAGGAGCCCCAGGGGGCGCGAGCCCCGCATGAATCATTGTAGTCAATCATTTT
 CCAGTTCTCAGCCGCTCAGTTGTGATCAAGGACACGTGGTTTCCGAAGTCCAGAGCTCAGAA
 TAGGAAAATAACTTGGGATTTTATATTGGAAGACATGGGATCTTGCTGCCAACGAGATCAGCA
 TTTATGACAAACTTTCAGAGACTGTTGATTTGGTGAGACAGACCGGCCATCAGTGTGGCATG
 TCAGAGAAGGCAATTGAAAAATTTATCAGACAGCTGCTGGAAAAGAATGAACCTCAGAGACC
 CCCCCGCGAGTATCCTCTCCTTATAGTTGTGTATAAGGTTCTCGCAACCTTGGGATTAATCT
 TGCTCACTGCCTACTTTGTGATTCAACCTTTAGCCCCATTAGCACCTGAGCCAGTGCTTTCT
 GGAGCTCACACCTGGCGCTCACTCATCCATCACATTAGGCTGATGTCCTTGCCCATTGCCAA
 GAAGTACATGTCAGAAAATAAGGGAGTTCTCTGCATGGGGGTGATGAAGACAGACCTTTC
 CAGACTTTGACCCCTGGTGGACAAACGACTGTGAGCAGAATGAGTCAGAGCCCATTCCTGCC
 AACTGCAGTGGCTGTGCCCAGAAACACCTGAAGGTGATGCTCCTGGAAGACGCCCCAAGGAA
 ATTTGAGAGGCTCCATCCACTGGTGATCAAGACGGGAAAGCCCTGTGGAGGAAGAGATTC
 AGCATTTTTTGTGCCAGTACCCTGAGGCGACAGAAGGCTTCTCTGAAGGGTTTTTCGCCAAG
 TGGTGGCGCTGCTTTCCTGAGCGGTGGTTCCCATTTCTTATCCATGGAGGAGACCTCTGAA
 CAGATCACAAATGTTACGTGAGCTTTTTCTGTTTTCTACTCACCTGCCATTTCCAAAAGATG
 CCTCTTTAAACAAGTGCTCCTTTCTTACCCAGAACCTGTTGTGGGGAGTAAGATGCATAAG
 ATGCCTGACCTATTTATCATTGGCAGCGGTGAGGCCATGTTGCAGCTCATCCCTCCCTTCCA
 GTGCCGAAGACATGTGCAGTCTGTGGCCATGCCAATAGAGCCAGGGGATATCGGCTATGTCG
 ACACCACCCACTGGAAGGTCTACGTTATAGCCAGAGGGGTCCAGCCTTTGGTCATCTGCGAT
 GGAACCGCTTTCTCAGAACTGTAGGAAATAGAAGTGTGCACAGGAACAGCTTCCAGAGCCGA
 AAACCAGGTTGAAAGGGGAAAAATAAAAAACAAAACGATGAAACTGCAAAA

FIGURE 20

MDLAANEISIIYDKLSETVDLVRQTGHQCGMSEKAIEKFIRQLLEKNEPQRPPPYPLLIVVY
KVLATLGLILLTAYFVIQPFSPLAPEPVLSGAHTWRSIIHHIRLMSLPIAKKYMSENKGVPL
HGGDEDRPFPDFDPWWTNDCEQNESEPIPANCTGCAQKHLKVMLLEDAPRKFERLHPLVIKT
GKPLLEEEIQHFLCQYPEATEGFSEGGFFAKWWRCFPERWFFFPYPWRRPLNRSQMLRELFV
FTHLPFPKDALNKCSEFLHPEPVVGSKMHKMPDLFIIGSGEAMLQLIPPFQCRRHCSVAMP
IEPGDIGYVDTHHWKVYIARGVQPLVICDGTAFSEL

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FIGURE 21

CCACGGTGTCGGTTCTTCGCCCCGGCGGCAGCTGTCCCCGAGGCGGGAGGAGCCCAGGGGGCG
CGAGCCCCGCATGAATCATTGTAGTCAATCATTTTCCAGTTCTCAGCCGTTCAGTTGTGATC
AAGGGACACGTGGTTTTCCGAAGTGCAGCTCAGAATAGGAAAATAACTTGGGATTTTATATT
GGAAGACATGGATCTTGCTGCCAACGAGATCAGCATTTATGACAACTTTAGAGACTGTTG
ATTTGGTGAGACAGACCGCCATCAGTGTGGCATGTCAGAGAAGGCAATTGAAAAATTTATC
AGACAGCTGCTGGAAAAGAAATGAACCTCAGAGACCCCCCGCAGTATCCTCTCCTTATAGT
TGTGTATAAGGTTCTCGCAACCTTGGGATTAATCTTGCTCACTGCCTACTTTGTGATTCAAC
CTTTCAGCCCATTAGCACCTGAGCCAGTGCTTTGTGGAGCTCAC

FIGURE 22

CCCACGCGTCCGCCACGCGTCCGGCTGAACACCTCTTCTTTGGAGTCAGCCACTGATGAGG
 CAGGGTCCCCACTTGCAGCTGCAGCAGCTGCAGCAGCTGCAGAGCGCTGCTCCTGGCTGGTG
 CCAGCTGGTGGCAGCGTGCCTAGACCGTGCCCTATGAGCCGTGGGGCTGCAGTGGGGAGCTGCC
 CTCCCTGCCGACCCACCAATGGCAGCCCCACCTTCTTTTGAAGACTTCCAGGCTTTTTGTGCCA
 CACCCGAATGGCCAGCTTCATCGACAACAGGTACAGCCAAC**ATG**TCCAGCTTCGAAATG
 GACACGCTATGCTAAGAGCCACGACCTTATGTCAAGTTTCTGGAATGCTGCTATGACATGCT
 TATGAGCAGTGGCGAGCGGCCAGTGGGAGCGGCCCCAGAGTCTCGGGCCTTCCAGGAGC
 TGGTCTGTGAACCTGCCGAGAGCGGGCGCGCTGGAGGGGCTACGCTACACGGCAGTGTCTG
 AAGCAGCAGCGAACCGACACTCCATGGCCCTGCTGCACCTGGGGGGCGCTGTGGCGCCAGCT
 CGCCAGCCCATGTGGGGCCTGGCGCTGAGGGACACTCCCATCCCCGCTGGAACCTGTCCA
 CGCCCGAGACATATTACGCATGCGCTCTGAAGCTGGTGCCCAACCATCTTCGACCCTCAC
 CTGGAAAGCAGCGCTCTCCGAGACAACTCTGGGTGAGGTTCCTCCTGACACCCACCGAGGAGGC
 CTCACCTGCTCTGGCAGTGACCAAAGAGGCCAAAGTGAGCACCCACCCGAGTTGCTGCAGG
 AGGACAGCTCTCGCGAGGACGAGCTGGCTGAGCTGGAGACCCCGATGGAGGCGAGCAGAAGT
 GATGAGCAGCTGAGAAGCTGTGTCTGTCCGCCGAGTGCCAGCTGGTGACGGTAGTGCCGT
 GGTCCACGGCTCTGAGAGTGCACACAGAAATGTATACTTCTACGATGGCAGCACTGAGC
 GCGTGGAAACCGGAGGAGGCTATGGCTATGATTTCCGGCGCCACTGGCCAGCTGCTGTGAG
 GTCCACTTCCCTCACTTCCCATGCAAGGTGGGCACGACCCAGTCTCTTATCTCTAGCCAGA
 CTCGAGACCCCGAGCTGGCCCCATCCCAACCCATACCCAGCTACGGAACCAAGGTGTACTCTG
 TGCTCTGCGCTACGGCCTACGGCCCCCTCTCAAGGCTACCTAAGCAGCCGCTCCGCCAGGAGAT
 TGTGCTGCTCAGGCCATTACCGAGAAATGGGTACAGCGTGAGATTAACAACCTTCAGTACT
 TGTGCAACTCAACACCATTTGCGGGCGGACCTACAATGACCTGTCTCAGTACCCCTGTGTTCT
 CCTGGCTCTCGAGGACTACGTGTCCCCAACCCCTGGACCTCAGCAACCCAGCCGCTTCCCG
 GGACCTGTCTTAAGCCCATCGGTGTGGTGAACCCCAAGCATGCCAGCTCGTGAGGGAGAAGT
 ATGAAAGCTTTGAGGACCCAGCAGGAGCAATTGACAAGTTCCACTATGGCAACCCCACTACTCC
 AATCGCAGGCGTGATGCACCTACCTCATCCGCGTGAGCCCTTACCTCCCTGCAGCTGCCA
 GCTGCAAAAGTGGCGCTTTGACTGCTCCGACCGGCAGTTCCACTCGGTGGCGGCAGCCTGGC
 AGGCACGCCCTGGAGAGCCTGCCGATGTGAAGGAGCTCATCCCGGAATTTCTTACTTTCCCT
 GACTTCTTGAGAAACAGAACGGTTTTGACCTGGGCTGTCTCCAGCTGACCAACGAGAAGGT
 AGCGATGTGGTGCTACCCCGTGGGCCAGCTCTCCTGAGGACTTCATCCAGCAGCACCGCC
 AGGCTCTGGAGTCGGAGTATGTGTCTGCACACCTACACGAGTGGATCGACCTCATCTTTGGC
 TACAAGCAGCGGGGGCCAGCCGCCGAGGAGGCCCTCAATGTCTTCTATTATGCACCTATGA
 GGGGGCTGTAGACCTGGACCATGTGACAGATGAGCGGGAACGGAAGGCTCTGGAGGGCATTA
 TCAGCAACTTTGGGCAGACTCCCTGTCAAGTGTGAAGGAGCCACATCACTCACTCGGCTCTCA
 GCTGAGGAAGCAGCCCATCGCCTTGCAAGCTGGACACTAATCACTACCTAGCATCTCCAGCA
 CTTGGAGCAACTCAAGCAATCTTCGACAGAGTCACTGTGAGTGCCAGTGCGGCTGTGGGGA
 CCCACAGCTGGTTGCCCTATGACCGCAACATAAGCAACTACTTCAGCTTCAGCAAAAGACCCC
 ACCATGGGACCGCCACAAGCAGCGCACTGCTGAGTGCCCGTGGGTGCGAGGCAAGTGGTGT
 GAGTGGACAAGCACTGGCAGTGGCCCCGGATGGAAGCTGCTATTTCAGCGGTGGCCACTGGG
 ATGGCAGCCTGGCGGTGCTGCACTACCCCGTGGCAAGCTGTTGAGCCAGCTCAGCTGCCAC
 CTTGATGATGTAACTGCGCTTGCACTGGACACCTGTGGCCTACTACCTCATCTCAGGCTCCCG
 GGACACAGCTGCTGATGGTTGGCGGCTCCTGCAATCAGGCTGGTCTGTGAGTGGCCTGGCAC
 CAAAGCTGTGCGAGTCTGTATGGGCACTGGGGCTGCAGTGAGCTGTGTGGCCATCAGCAT
 GAACTTGACATGGCTGTGTCTGAGATCTGAGGATGGAACCTGTGATACACATGTACCGCG
 CGGACAGTTTGTAGCGGCACACGCGCTCTGGGTGCCACATTCCTTGGACCTATTTTCCACC
 TGGCATTTGGGTTCGGAAGCCAGATTGTGGTACAGAGCTCAGCGTGGGAGCGTCTGGGGCC
 CAGGTCACTTACTCTTGCACTGTATTGAGTCAATGGGAAGTTGGCGGCTCTACTGCCCCCT
 GGCAGAGCAAGCTCAGCGCTGACGGTGACAGAGGACTTGTGTTGCTGGGACCGCCGCACT
 GCGCCCTGCACATCTCAACTAAACACACTGCTCCCGCGCCGCGCTCCCTTGCCCATGGAAG
 GTGGCCATCCGACAGCTGGCCGTGACCAAGGAGCGCAGCCGCTGTGGTGGGCTGGAGGA
 TGGCAAGCTCATCTGTTGGTGTGCGGGGGCAGCCCTCTGAGGTGGCGAGCAGCGAGTTGCGCG
 GGAAGCTCTGCGCGCTCTGCGCGCATCTCCAGGTTCTCTCGGAGAGCAGCGAATAACAAC
 CCTACTGAGGCGCGC**TGA**ACTGGCCAGTCCGGCTGCTCGGGCGCGCCGCCCCGGCAGGCGCT
 GCGCGGAGGCGCCCGCAGAAGTCCGCGGGGAACACCCGGGGTGGGACCGGAGGGGTGA
 GCGGGGCCCAACCTCCCAAGCTCAGGAGTTGGCGGGCATGTTACCCCTCAGGAGTTGGCG
 GCGGGAAGTCCCGCTGCGCGCTGAGGGCGCGCCTGAGTGGCCAGCATGGCGCT

FIGURE 23

MSQFEMDITYAKSHDLMSGFWNACYDMLMSSGQRRQWERAQSRRAFQELVLEPAQRRLARLEGL
 RYTAVLKQQAQTQHSMLLHWGALWRQLASPCGAWALRDTPIPRWKLSSAETYSRMRLKLVPN
 HHFDPHLEASALRDNLGEVPLTPTEEASLPLAVTKEAKVSTPPELLQEDQLGEDELALEETP
 MEAAELDEQREKLVLSAECQLVTVVAVVPGLLEVTTQNVYFYDGSSTERVETEEGIGYDFRRP
 LAQLREVHLRRFNLRRSALELFFIDQANYFLNFPCKVGTTPVSSPSQTPRPQFGPIPPHTQV
 RNQVYSWLLRLRPPSQGYLSSRSPQEMLRASGLTQKWVQREISNFEYLMQLNTIAGRTYNDL
 SQYPVFVFWLQDYVSPDLDSNPAVFRDLSPKIGVVNPKHAQLVREKYESFEDPAGTIDKFH
 YGTHYSNAAGVMHYLIRVEPFTSLHVQLQSGRFDCSDRQFHSVAAAWQARLESADVKELIP
 EFFFYFPDFLENQNGFDLGLCLQLTNEKVGDVVLPFWASSPEDFIQHQHRALESEYVSAHLHEW
 IDLIFGYKQRGPAAEEALNVFYCYEGAVDLDHVTDERERKALEGIIISNFGQTPCQLLKEP
 HPTRLSAEEAAHRLARLDTNSPSIFQHLDELKAFFAEVTVSASGLLGTHSWLPYDRNISNYF
 SFSKDPMTGSHKTRQLLSGPVWPGSGVSGQALAVAPDGKLLFSGGHWGDSLRTALPRGKLL
 SQLSCHLDVVTCLALDTCGIIYISGSRDTCMVWRLHLQGGLSVGLAPKPVQVLYHGAAVS
 CVAISTELDMAVSGSEDTGTVIIHTVRRGQFVAALRPLGATFFGPIFHLALGSEGQIVVQSSA
 WERPGAQVTVSYLHLYSVNGKLRASLPLAEQPTALTVTEDFVLLGTAQCALHILQLNTLLPAA
 PPLPMKVAIRSVAVTKERSHVLVGLLEDGKLIVVVAGQPSEVRSSQFARKLWRSSRRISQVSS
 GETEYNPTAR

N-glycosylation site.

amino acids 677-681

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 985-989

Tyrosine kinase phosphorylation site.

amino acids 56-65, 367-376, 543-551

N-myristoylation site.

amino acids 61-67, 436-442, 604-610, 610-616, 664-670, 691-697,
 706-712, 711-717, 769-775, 785-791, 802-808, 820-826, 834-840,
 873-879, 912-918, 954-960

FIGURE 24

CGGACGCGTGGGCGGACGCGTGGGGGCTGTGAGAAAGTGCCAATAAATACATCATGCAACCC
 CACGGCCACCTTGTGAATCCTCGTGCCACGGGCTGATGTCGTCTTCCAGGGCTACTCAT
 CCAAAGCCCTAATCCAACGTTCTGTCTTCAATCTGCAAATCTATGGGGTCTTGGGGCTCTTC
 TGGACCCCTTAATCTGGGTACTGGCCCTGGGCCAATGCGTCTCGTGGAGCCTTTGCCTCCTT
 CTACTGGGCCTTCCACAAGCCCCAGGACATCCCTACCTTCCCCTTAATCTCTGCCTTCATCC
 GCACACTCCGTTACCACACTGGGTCAATTGGCATTGGAGCCCTCATCTGACCCTTGTGCAG
 ATAGCCCGGGTCATCTTGGAGTATATTGACCACAAGCTCAGAGGAGTGCAGAACCCCTGTAGC
 CCGCTGCATCATGTGCTGTTTCAAGTGCTGCCTCTGGTGTCTGGAAAAATTTATCAAGTTCC
 TAAACCGCAATGCATACATCATGATCGCCATCTACGGGAAGAATTTCTGTGTCTCAGCCAAA
 AATGCGTTCATGCTACTCATGCGAAACATTGTCAGGGTGGTCTGCTGGACAAAGTCACAGA
 CCTGTGTGCTGTTCTTTGGGAAGCTGCTGGTGGTCTGGAGGCGTGGGGGTCTGTCTCTTTT
 TTTTCTCCGGTCGCATCCCGGGCTGGGTAAAGACTTTAAGAGCCCCACCTCAACTATTAC
 TGGCTGCCCATCATGACCTCCATCCTGGGGGCCCTATGTCATCGCCAGCGGCTTCTTCAGCGT
 TTTCGGCATGTGTGTGGACACGCTCTTCTCTGCTTCTGGAAGACCTGGAGCGGAACAACG
 GCTCCCTGGACCGGCCCTACTACATGTCCAAGAGCCTTCTAAAGATTCTGGGCAAGAAGAAC
 GAGGCGCCCCCGGACAACAAGAAGAGGAAGAAGTGAAGCAGCTCCGGCCCTGATCCAGGACTGC
 ACCCCACCCACCGTCCAGCCATCCAACCTCACTTCGCCTTACAGGTCTCCATTTTGTGGT
 AAAAAAGGTTTTAGGCCAGGCGCGTGGCTCACGCCTGTAATCCAACACTTTGAGAGGCTG
 AGGCGGGCGGATCACCTGATCAGGAGTTCGAGACCAGCCTGGCCAACATGGTGAAACCTCC
 GTCTCTATTAATAAATACAAAATTAGCCGAGAGTGGTGGCATGCACCTGTCTATCCAGCTAC
 TCGGAGGCTGAGGCAGGAGAATCGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAGCCGAGA
 TCGCGCCACTGCACTCCAACCTGGGTGACAGACTCTGTCTCCAAAACAAAACAAACAA
 AAAGATTTTATTAAAGATATTTTGTTAAGTCT

FIGURE 25

RTRGRTRGGCEKVPINTSCNPTAHLVNSSCPGLMCFVQGYSSKGLIQRSVFNLQIYGVGLGF
 WTLNWWLALGQCVLAGAFASFYWAFHKPQDIPTFPLISAFIRTLRYHTGSLAFGALILTLVQ
 IARVILEYIDHKLRGVQNPVARCIMCCFKCCLWCLEKFIKFLNRNAYIMIAIYGKNFCVSAK
 NAFMLLMRNIVRVVLDKVTDLLLFFGKLLVVGVGVLSEFFFFSGRIPGLGKDFKSPHLNYY
 WLPIMTSILGAYVIASGFFSVFGMCVDTLFLCFLEDLERNNGSLDRPYMSKSLLKILGKKK
 EAPPDNKKRKK

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FIGURE 26

GAGTCTTGACCGCCGCCGGGCTCTTGGTACCTCAGCGCAGCGCCAGGCGTCCGGCCGCCGT
 GGCT**ATG**TCGTGTCGGATTTCCGCAAAGAGTTCTACGAGGTGGTCCAGAGCCAGAGGGTCC
 TTCTCTTCGTGGCCTCGGACGTGGATGCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTT
 CAGTGTGACCACTGCAATATACGCTGGTTCCAGTTTCTGGGTGGCAAGAAGTTGAACTGTC
 ATTTCTTGAGCATAAAGAACAGTTTCATTATTTTATTCTCATAACTGTGGAGCTAATGTAG
 ACCTATTGGATATTCTTCAACCTGATGAAGACACTATATTCTTTGTGTGACTCCCATAGG
 CCAGTCAATGTCGTCAATGTATACAACGATACCCAGATCAAATTACTCATTAAACAAGATGA
 TGACCTTGAAGTTCCCGCCTATGAAGACATCTTCAGGGATGAAGAGGAGGATGAAGAGCATT
 CAGGAAATGACAGTGTGGGTGAGAGCCTTCTGAGAAGCGCACACGGTTAGAAGAGGAGATA
 GTGGAGCAAACCATGCGGAGGAGGCAGCGCGAGAGTGGGAGGCCGGAGAAGAGACATCCT
 CTTTGACTACGAGCAGTATGAATATCATGGGACATCGTCAGCCATGGTGATGTTTGAGCTGG
 CTTGGATGCTGTCCAAGGACCTGAATGACATGCTGTGGTGGGCCATCGTTGGACTAACAGAC
 CAGTGGGTGCAAGACAAGATCACTCAAATGAAATACGTGACTGATGTTGGTGTCTGCAGCG
 CCACGTTTCCCGCCACAACACCACCGGAACGAGGATGAGGAGAACACACTCTCCGTGGACTGCA
 CACGGATCTCCTTTGAGTATGACCTCCGCCTGGTGCTCTACCAGCACTGGTCCCTCCATGAC
 AGCCTGTGCAACACCAGCTATACCGCAGCCAGGTTCAAGCTGTGGTCTGTGCATGGACAGAA
 GCGGCTCCAGGAGTTCCTTGACAGACATGGGTCTTCCCTGAAGCAGGTGAAGCAGAAAGTTCC
 AGGCCATGGACATCTCCTTGAAGGAGAATTTGCGGGAAATGATTGAAGAGTCTGCAAAATAAA
 TTTGGGATGAAGGACATGCGCGTGACACTTTTTCAGCATTCTTTTGGGTTCAGCACAAGTT
 TCTGGCCAGCGACGTGGTCTTTGCCACCATGTCTTTGATGGAGAGCCCCGAGAAGGATGGCT
 CAGGGACAGATCACTTATCCAGGCTCTGGACAGCCTCTCCAGGAGTAACCTGGACAAGCTG
 TACCATGGCCTGGAACCTGCACAAGAAGCAGCTGCGAGCCACCCAGCAGACCATTTGCCAGCTGC
 CTTTGCACCAACCTCGTCATCTCCAGGGCCTTTCTGTACTGCTCTCTCATGGAGGGCAC
 TCCAGATGTCATGCTGTTCTCTAGGCCGGCATCCCTAAGCCTGCTCAGCAAACACCTGCTCA
 AGTCTTTGTGTGTTTCGACAAAGAACCGCGCTGCAAAGCTGCTGCCCTGGTGATGGCTGCC
 CCCCTGAGCATGGAGCATGGCACAGTGACCGTGGTGGGCATCCCCCAGAGACCGACAGCTC
 GGACAGGAAGAACTTTTGGGAGGGCGTTTGAGAAGGCAGCGGAAAGCACCAGCTCCCGGA
 TGCTGCAACAACATTTTGACCTCTCAGTAATTGAGCTGAAAGCTGAGGATCGGAGCAAGTTT
 CTGGACGCATTATTTCCCTCCTGTCT**TAG**GAAATTTGATTCTTCCAGAATGACCTTCTTATT
 TATGTAAGTGGCTTTCATTTAGATTGAAGTTATGGACATGATTGAGATGTAGAAGCCATT
 TTTTATTAAATAAATGCTTATTTTAGGAAA

FIGURE 27

MFVSDFRKEFYEVVQSQRVLLFVASDVDALCACKILQALFQCDHVQYTLVPVSGWQELETAF
 LEHKEQFHYFILINCGANVDLLDILQPD EDTIFFVCDSHRPVNVVNVYNDTQIKLLIKQDDD
 LEVPAYEDI FRDEEED EHS GNDSDGSEPS EKRTL EEEIVEQTMRRRQRREWEARRRDILF
 DYEQYEHGTSSAMVMFELAWMLSKDLNDMLWVAIVGLTDQWVQDKITQMKYVTDVGVLQRH
 VSRHNRNEDEENTLSVDCTRISFEYDLRLVLVYQHWSLHDSL CNTSYTAARFKLWSVHGQKR
 LQEFLADMGLPLKQVKQKQFQAMD ISLKENLREMI EESANKFGMKDMRVQTF SIHFGFKHKFL
 ASDVVFATMSLMESPEKDGSGTDHFIQALDSLRSRNL DKLYHGLELAKKQLRATQQTIASCL
 CTNLVISQGPFLYCSLMEGTPDVMLFSRPASLSLLSKHLLKS FVCSTKNRRCKLLPLVMAAP
 LSMEHGTVTVVGI PPETDSSDRKNFFGRAFEKAAESTSSRMLHNHFDLSVIELKAEDRSKFL
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FIGURE 28

GTACCTCAGCGCGAGCGCCAGGCGTCCGGCCGCCGTGGCTATGNTCGTGTCCGATTTCCGCA
 AAGAGTTTCTACGAGGTGGTCCAGAGCCAGAGGGTCCTTCTCTTCGTGGCCTCGGANGTGGAT
 GCTCTGTGTGCGTGCAAGATCCTTCAGGCCTTGTTCCAGTGTGACCANGTGCAATATANGCT
 GGTTCAGTTTTCTGGGTGGCAAGAAGTGAAGTGCATTTCTTGAGCATAAAGAACAGTTTC
 ATTATTTTATTCTCATAAACTGTGGAGCTAATGTAGACCTATTGGATATTCTTCAACCTGAT
 GAAGACACTATATTCTTTGTGTGTGACCCCATAGGCCAGTCAATGTTGTCAATGTATACAA
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FIGURE 29

CAGGAACCCCTCTCTTTGGGTCTGGATTGGGACCCCTTTCCAGTACCATTTTTTTCTAGTGAAC
 CACGAAGGCGCATACAGAAAAACCCCTCAACCCAAAGGAAATAGACTACAGCCCCAATTG
 GGTGACTTTGGCTATAGAAAAAGAAAGGAACGAAAAAGACAGTTTTTTTTGGAAAGCTAA
 GTCCTTCCCTTTATCGAGTCAAGAAACCCCCCTTCTTGAGCTATTTACAGCTTTTAAACAAAT
 GAGTAAAGTACGCTCCGGTCAAC**ATGG**GTGACAGCGCCCTGGTCCCGTCTGGGCGAGCGTCT
 CTGCTCTTTCTCTCTGATGTGTGAGATCCGATGGTGGAGTCACTTTTGACAGAGTCTGGGC
 CAGCGCTGCTCCAGCGTCTGCTGACTCTGAGGACCCCTGGATCCTGCCATGTATCTCTCAG
 CCTCTTCCCTCCGGCCGCCCCACGCCCTGGCTGAGATCAGACCTACATTAAATATCACCATC
 CTGAAGGGTGACAAAGGGGACCCAGGCCCAATGGGCTGCCAGGTACATGGGCGAGGGAGG
 TCCCAAGGGGAGCCCTGGCCCTCAGGCGAGCAAGGGTGACAAGGGGGAGATGGGCGAGCCCCG
 GCGCCCGGTGCCAGAAAGCGCTTCTTTCGCTTCTCAGTGGGCCGAGAAGCGGCCCTGCACAGC
 GCGGAGGACTTCCAGACGCTGCTCTTCGAAAGGGTCTTTGTGAACCTTGATGGGTGCTTTGA
 CATGGCGAGCGGCCAGTTTGTCTGCTCCCTGCGTGGCATCTACTTCTCAGCCTCAATGTGC
 ACAGCTGGGAATTACAAGGAGACGTACGTGCACATTATGCAATAACCAGAAAGAGGCTGTCTATC
 CTGTACCGCGAGCCAGCGAGCGCAGCATCATCAGAGCCAGAGTGTGATGCTGGACCTGGC
 CTACGGGACCGCGTCTGGGTGGCGCTCTTCAAGCGCCAGCGCGAGAAGCGCATCTACAGCA
 ACGACTTGCACCTACATCACCTTCAAGCGGCCACCTCATCAAGGCCGAGGACGA**CTGA**GGG
 CCTCTGGGCCACCTCCCGGCTGGAGAGTCAAGGTGCTGGTCCCGTCCCTGCAGGGCTCAG
 TTTGCACTGCTGTGAAGCAGGAAGGCCAGGGAGGTCCCGGGGAGCTGGCATCTCGGGGAGA
 CCCTGCTTCTTCTTGGCTGCCATCATCCCTCCAGGCTATTTCTGCTCCTCTCTCTCTCT
 TGGACCTATTTTAAAGACTTGCTAACCATAAATATTCTAGAAGTTCCAGAGCTCGTAGGCC
 AGCACTTCTCAAATCTGGAAATGCATGCGAATCACCCGGGGTTCGTGTTAAATGACAGATTCT
 GACTCAGCAGGTCTGAGTGGGTCCAGGATTCTGTGTTTCTCATATGTTCTGGGTGATGCTG
 ATGGGTCAGTCTATGAACCACTGGAGCAACCAAGTTCTAGGACTTTCTCAATATTCTAG
 TACTTCTGAACATTCTGGAAATCTCCCAACATTCTAGAATTCTCCCAACATTTTTTTTTCT
 TGAGACAGAGTCTTGGCTCTGTGTGCCAGGCTAGAGTGCAGTGGTGCAATCTCAGTTCACTGC
 AACCTCTGCCCTCCCGGGTTCAGCGATTCTTCTGCCCTCAGCTCCTCAGTGGGTGGGATTAC
 AGGCGGCTGCTACCATGCTCGGTGCTAATTTTGTATTTTGTAGTAGAGATGGGGTTTACCAATA
 TTGGCCAGGTGGTCTTGAAGTCTCTGACTTCAGGTGACCCACCGGCTCGGCCCTCTCAAAAT
 GCTGGGATTACAGGTGTGAGCCACCGTGCTGGCCAAATTCACAACTTCTTAAATTTCTCAT
 CCCTCCAGGGTCCCGGTGCTATGTTCTCTTTACCCCTTCCCGCTCTCTCTGCTCAGGCC
 TGCACCACTCAGGCCACCGTTCATTTATTATTATTAAACACTGAGCACTCACTCTGTGGCT
 GGGTCCCGGAGGGGTGAGGGGGTCAGACACAGGCCCTGCCCTCAGTCACTGAGTGGGCCA
 GTCCAGCCAGGCCGGGAGAGATGTGTACATAGGTTTTAAAGCAGACCAGAGACTCATGGGG
 GCTCTGTGTTCTGGGTGTTTCAGGTGCTGCTGGTCTCCATTACCCTGCTCCCCAAGGCTGG
 TGGGACGGGGTCCCGGTGGCAGGGGCGAGTATCTCCTTCCCGTCTCTCATCCACCTGCCAG
 TGCTCATCTGCTACAGCAACCCAGGGGGCTTGGCCAGGTCAAGGGTTCTGTGAGGAGAGG
 ACCCCAGGAGTGTGGGGCATTTTGGGGGGTGAAGTGGCCCCGGAAGATGGAACCCACACCCA
 TAGCTCTCCCCAGCTGATACGGCATCTGCGAGAAGACCTGCCCTCCTCACTGGGATCCC
 CTTCTCGCTCTCTCCAGGGCTCTGCCAGGGCCTTGCTCAGTTCCTTCCACCAAGTCACTCT
 GAACTCCGGTTTCCCAAGGGCTCCAGCTGCCCTCAGACACTGATGTCTGTGCCAGGTGGT
 CTCCTGCCCTCATGCCCTCTCACCGGCCAGTGCCCCGACTCTCCAGGCTTTATCAAGGTG
 CTAAGGCCGGGTGGGCGAGTCTCGTCTCAGAGCCCTCCTCCGGCTGGTGTGCTGCTTTAC
 AAACACTGCAGGAGAAGGGCCACGGAAGCCCAAGGCTTTAGAGCCCTCAGCAGGTCTGGGG
 AGCTAGAGCAAGGAGGACCTCAGGCCCTTCCGTTTCTTCTCCAGGGTGGGTGGCTGGT
 GTTCCCCTAGCTTCCAACCCAGGTGGCTGCCCTTCTCCCCAGGAGGGGGCTCCGC
 CCATTGGTGCTCATGCAACTCTGGGGCTGAGGTGCCCGGGGGTGATCTGTGGTGCTCAC
 AGCCGAGGGAGCCGTGGCTCCATGGCCAGATGACGGAAACAGGGTCTGACCAAGTGCCAGGA
 AGACCTGTGCTATAAACACCCCTGCGTATCTTCCCTGCTGACCCGCCACCGCTGCC
 GTCCAGCATGATTAAGAATGCTGTCTCTCTTGGAAAAA

FIGURE 30

MVTAALGPVWAAALLFLLMCEIRMVELTFDRAVASGCQRCDDSEDLDPAHVSSASSSSGRPH
ALPEIRPYINITILKGDKGDPGPMGLPGYMGREGPQGEPPQGSKGDKGEMGSPGAPCQKRF
FAFSVGRKTALHSGEDFQTLLEFRVFNLDGCFDMATGQFAAPLRGIYFFSLNVHSWNYKET
YVHIMHNQKEAVILYAQPERSIMQSQSVMLDLAYGDRVVWRLFKRQRENAIYSNDFDTYIT
FSGHLIKAEDD

Important features:

Signal peptide:

amino acids 1-20

N-glycosylation site.

amino acids 72-75

Clq domain proteins.

amino acids 144-178, 78-111 and 84-117

FIGURE 31

ACTCGAACGCAGTTGCTTCGGGACCCAGGACCCCTCGGGCCCCGACCCGCCAGGAAGACTG
 AGGCCCGGGCCTGCCCGCCCGGCTCCCTGCGCCGCCCGCCCTCCGGGACAGAAAGACTG
 CTCACGGGTCCCTCTGCTGCTGCCGTGCTCCTGCTACTGGCCCTGGGGCTGGGGTGACGG
 GCTGCCATCCGGCTGCCAGTGCAGCCAGCCACAGACAGTCTTCTGCACTGCCCGCCAGGGG
 ACCACGGTGCCCCGAGACGTGCCACCCGACACGGTGGGGCTGTACGTCTTTGAGAACGGCAT
 CACCATGCTCGAGCGAGGCAGCTTTGCCGGCTGCCGGGCTGCAGCTCCTGGACCTGTAC
 AGAACCATGTCGCCAGCTGCCAGCGGGCTTCCAGCCATGCCAACCTCAGCAACCTG
 GACCTGACGGCCAAACAGGCTGCATGAAATCACCAATGAGACCTTCCGTGGCTGCCGGCCT
 CGAGCGCTCTACCTGGGCAAGAACCGCATCCGCCACATCCAGCTGGTGCCTTCGACACGC
 TCGACCGCCTCCTGGAGCTCAAGCTGCAGGACAACGAGCTGCGGGCACTGCCCCGCTGCGC
 CTGCCCGCCTGCTGCTGCTGGACCTCAGCCACAACAGCCTCCTGGCCCTGGAGCCCGGCAT
 CCTGGACACTGCCAACCTGGAGGCGCTGCGGGCTGGCTGGTCTGGGGCTGCAGCAGCTGGACG
 AGGGGCTCTTTCAGCCGCTTGCGCAACCTCCAGACCTGGATGTGTCCGACAACAGCTGGAG
 CGAGTGCCACCTGTGATCCGAGGGCTCCGGGGCTGACGCGCTGCGGCTGGCCGGCAACAC
 CCGCATTGCCAGCTGCGGCCCGAGGACCTGCGCGGCTGGCTGCCCTGCAGGAGCTGGATG
 TGAGCAACCTAAGCCTGCAGGCCCTGCCCTGGCGACCTCTCGGGCTCTTCCCGCCGCTGCGG
 CTGCTGGCAGCTGCCCGCAACCCCTTCAACTGCGTGTGCCCTCAGTGTGGTGTGGCCCTG
 GGTGCGCGAGGACACGTGCACACTGGCCAGCCCTGAGGAGACGCGCTGCCACTTCCGCCCCA
 AGAACGCTGGCCGGCTGCTCCTGGAGCTTGACTACGCCACTTTGGCTGGCCAGCCACACACC
 ACCACGTCACAGTGGCCACACAGGCGCCGTGGTGGGGAGCCCAAGCCACTTGTCTTCTAG
 CTTGGCTCCTACCTGGCTTAGCCCCACAGCGCCGGCCACTGAGGCCCCAGCCCGCCCTCCA
 CTGCCCCACGCACTGTAGGGCTGTCCCCAGCCCCAGGACTGCCACCGTCCACCTGCCTC
 AATGGGGGACATGCCACCTGGGGACACGGCACCACTGGCGTGTGTGTGCCCGAAGGCTT
 CACGGGCTGTACTGTGAGAGCCAGATGGGGCAGGGGACACGGCCAGCCCTACACCACTCA
 CGCCGAGGCCACCAAGCTCCTGACCTGGGCATCGAGCCGTTAGCGCCACCTCCTTGCAGC
 GTGGGGCTGCAGCGCTACCTCCAGGGGAGCTCCGTGCAGCTCAGGAGCCTCCGTCTCACCTA
 TCGCAACCTATCGGGCCTGATAAGCGGCTGGTGACGCTGCGACTGCCTGCCTCGCTCGCTG
 AGTACACGGTCAACCAGCTGCGGCCCAACGCCACTTTACTCCGTGTGTGTATGCCTTTGGGG
 CCGGGCGGGTGCCGGAGGGCGAGGAGGCTGCGGGGAGGCCCATACACCCCCAGCCGCTCCA
 CTCCAACCAGCCCACTACCCAGGCCCGCGAGGGCAACCTGCAGCTCCTCATTTGCGCCCG
 CCTTGGCCGGGTGCTCCTGCGCGCTGGCTGCGGTGGGGGAGCCTACTGTGTGCGCGCG
 GGGCGGGCCATGGGAGCAGCGGCTCAGGACAAAGGGCAGGTGGGGCCAGGGGCTGGGCCCC
 GGAACCTGGAGGAGTGAAGGCTCCCTTGGAGCCAGGCCCAAGGCAACAGAGGGCGGTGGAG
 AGGCCCTGCCAGCGGGTGTAGTGTGAGGTGCCACTCATGGCTTCCAGGGGCTGGCCTC
 CAGTCAACCTCCACGCAAGCCCTACATCTAAGCCAGAGAGACAGGGCAGCTGGGCGCG
 GGCTCTCAGCCAGTGAGATGGCCAGCCCTCCTGTGCTGCCACACCACTGAAGTTCTCAGTCC
 CAACCTCGGGGATGTGTGCAGACAGGGCTGTGTGACCAAGCTGGGCCCTGTTCCCTTGGGA
 CCTCGGTCTCCTCATCTGTGAGATGCTGTGGCCAGCTGACGAGCCCTAACGTTCCCGAAGC
 CGAGTGCCATGAGGACAGTGTCCGCCCTGCCCTCCGCAACGTGCAGTCCCTGGGCACGGCG
 GGCCCTGCCATGTGCTGTGTAACGATGCTGGGTCTGTGCTGGGCTCTCCCACTCCAGGGCGGA
 CCTGGGGGCAAGTGAAGGAAGCTCCCGGAAAGAGCAGAGGGAGCGGCTAGGCGCGCTGTG
 TGACTCTAGTCTTGGCCCCAGGAAGCGAAGGAACAAAAGAACTGGAAGGAAGATGCTTTA
 GGAACATGTTTTGCTTTTTTAAATATATATATTTATAAGAGATCCTTTCCCATTTATCTG
 GGAAGATGTTTTTCAAACTCAGAGACAGGACTTGGTTTTGTAAGACAAACAGATGATAG
 AAGGCCCTTTTGTAAAGAAAAATAAAGATGAAGTGTGAAA

FIGURE 32

MCSRVLLLLLLLLLALGPGVQGCPSGCQCSQPQTVECTARQGTTVPRDVPDPDTVGLYVFEN
 GITMLDAGSFAGLPGLQLLDLSQNQIASLPSGVFQPLANLSNLDLTANRLHEITNETFRGLR
 RLERLYLGKNRIRHIQPGAFDTLDRLLELKLQDNELRALPPLRLPRLLLLDLSHNSLLALEP
 GILDANVEALRLAGLGLQQLDEGLFSRLRLNLDLDVSDNQLERVPPVIRGLRGLTRLRLAG
 NTRIAQLRPEDLAGLALQELDVSNLSLQALPGDLSGLFPRLRLAAARNPFNCVCPLSWFG
 PWVRESHVTLASPEETRCHFPFKNAGRLLLELDYADFGCPATTTTATVPTTRPVVREPTALS
 SSLAPTWLSPTAPATEAPSPSTAPPTVGPVPQPDCCPSTCLNGGTCHLGRHHLACLCPE
 GFTGLYCESQMGQTRPSPTPVTPRPPRSLTLGIEPVSPTSLRVGLQRYLQGSSVQLRSLRL
 TYRNLSGPDKRLVTLRLPASLAEYTVTQLRPNATYSVCMPLGPGRVPEGEEACGEAHTPPA
 VHSNHAPVTQAREGNLPLLIAPALAAVLLAALAAGVGAAYCVRGRAMAAAAQDKGQVGPAGAG
 PLELEGVKVPLEPGPKATEGGGEALPSGSECEVPLMGFPGPGLQSPLHAKPYI

FIGURE 33

GAATCATCCACGCACCTGCAGCTCTGCTGAGAGAGTGCAAGCCGTGGGGGTTTTGAGCTCAT
 CTTTCATCTTATATGAGGAAATAAAGTGGTAAAATCCTTGGAAATACA**AT**GAGACTCATCAG
 AAACATTTACATATTTTGTAGTATTGTTATGACAGCAGAGGGTATGCTCCAGAGCTGCCAG
 AAGAAAGGGAATCTGATGACCAACTGCTCCAACATGTCTCTAAGAAAGGTTCCCGAGACTTG
 ACCCGAGCCACACGACACTGGATTATTCCTATAACCTCCTTTTCACTCCAGAGTTGAGA
 TTTTCATTCTGTCTCCAACTGAGAGTTTGTATTCTATGCCATTAACAGAAATCAACAGCTGG
 ATCTCAAAAGCTTTGAATTTCAACAAGGAGTTAAGATATTTAGATTGTCTTAATAACAGACTG
 AAGAGTGTAACTTGGTATTTACTGGCAGGTCCTCAGGTATTTAGATCTTTCTTTTAACTGACTT
 TGACACCATGCTTATCTGTGAGGAAGCTGGCAACATGTACACCTGGAAATCCTAGGTTTGA
 GTGGGGCAAAATACAAAATCAGATTTCCAGAAAATTGCTCATCTGCATCTAAATCTGTCT
 TTCTTAGGATTCAGAACTCTTCCCTCATTATGAAGAAGGTAGCCTGCCCATTTAAACACAAC
 AAAACTGCACATTGTTTTACCAATGGACACAATTTCTGGGTTCTTTTGCCTGATGGAATCA
 AGACTTCAAAAATATTAGAAATGACAAATATAGATGGCAAAAGCCAATTTGTAAGTTATGAA
 ATGCCACGAAATCTTAGTTTATAGAAATGCTAAGACATCGGTTCTATTGCTTAATAAAGTTGA
 TTTACTCTGGACGACCTTTTCCCTTATCTTACAATTTGTTGGCATACATCAGTGGAACTAT
 TTCAGATCCGAAATGTGACTTTTGGTGGTAAGGCTTATCTTGACCACAATTCATTGACTAC
 TCAGATATCTGTAATGAGAACATATAAAATTTGGAGCATGTACATTTCCAGAGTGGTTTACATTC
 ACAGGATATAATCTATTGCTTTTGACCAAAATGGACATAGAAAACCTGCACATATCAAAATG
 CACAAATGTCACACACTGCTTTTCCGAAATATCCCTACGAAATTTCCAATTTTAAATTTTGGC
 AATAATATCTTAAACAGACGAGTTGTTTAAAGAACTATCCAACCTGCCTCATTGAAAACCTCT
 CATTTTGAATGACATAAACTGGAGACACTTTCTTAGTAAGTTGCTTGTGCTAACACACAC
 CCTTGGAACTCTGGATCTGAGTCAAAATCTATTACAACATAAAATGATGAAAATTTGCTCA
 TGGCCGAAACTGTGGTCAATTAAGATCTGTATACATAAAATTTGCTGATTTCTGTCTTCAG
 GTGCTTGCCCAAAAGTATTCAAATACTTGACCTAAATAATAACCAAAATCCAACTGTACCTA
 AAGAGACTATCTCATGTGAGGCTTACGAGAACTAAATATTGCATTTAAATTTCTAAGCTAT
 CTCCTCGGATCGAGTCAATTTGAGTAGACTTTGAGTTCTGAACATTGAATGAACCTCATTTCT
 CAGCCCATCTCTGGATTTTGTTCAGAGCTGCCAGGAAGTTAAACCTCTAAATGCGGGGAAGAA
 ATCCATTCGGGTGACCTGTGAATTAATAAAATTTCAATTCAGCTTGAAACATATTCAGAGGTC
 ATGATGGTTGGATGGTCAGATTTCATACACCTGTGAATACCTTTAAACCTAAAGGGGAACCTAG
 GTTAAAGAGCTTCATCTCCACGAATATCTTGCAACACAGCTCTGTTGATTGTCACCATTTG
 TGGTTATTATGCTAGTTCTGGGGTTGGCTGTGGCCCTCTGCTGTCTCCACTTTGATCTGCC
 TGGTATCTCAGGATGCTAGGTCAATGCACACAACATGGCACAGGGTTAGGAAAAACAACCA
 AGAACCACTCAAGAGAAATGTCCGATTCCACGCAATTTATTCATACAGTGAACATGATTTCT
 TGTGGGTGAAGAAATGAATTGATCCCCAATCTAGAGAAGGAAGATGGTTCTATCTTGATTTGC
 TTTTATGAAAGCTACTTTGACCTTGGCAAAAGCAATTAGTGAAAATATTGAGACCTTCATTGA
 GAAAAGCTATAAGTCCATCTTTGTTTGTCTCCCACTTTGTCCAGAATGAGTGGTGCCATT
 ATGAATTTACTTTTGGCCACCAACAATCTCTCCATGAAAATTTCTGATCATATAAATTTCTATC
 TTAAGTGAACCCATTTCCATTTCTATTGCATTTCCCAACAGGATCATATAAATGAAAGCTCTCCT
 GGAAAAAAGACATACCTTGGAAATGGCCCAAGGATAGGCGTAATGTGGGCTTTTCTGGGCA
 ACCTTCGAGTCTGCTATTAATGTGAATGTATTAGCCACAGAGAATATGATGAATCGCAGACA
 TTCACAGGTTAAATGAAGAGTCTCGAGTTCTACAATCTCTCTGATGAGAAGACAGATTGTCT
ATAAAATCCACAGTCTCTTGGGAAGTTGGGGACCACTACACTGTGGGATGTACATTTGATA
 CAACCTTTATGATGGCAATTTGACAATATTGATAAATAAAAAATGGTTATTCCTTCATA
 TCAGTTTCTAGAAGGATTTCTAAGAAATGTATCCTATAGAAAACCTTCAACAGTTTATAAGG
 GCTTATGGAAAAAGGTGTTCTCCCGAGGATTGTTTATAATCATGAAAATGTGGCCAGGTGC
 AGTGGCTCACTCTTGTAAATCCAGCACTATGGGAGGCGCAAGTGGGTGAGCCACAGAGGTCAA
 GAGATGGAGACCATCTCTGGCAACATGGTGAACCTGTCTCTACTAAAAATACAAAAATTA
 GCTGGGCGTGATGGTGCACGCTGTAGTCCAGCTACTTGGGAGGCTGAGGCCAGGAAGATCG
 CTTGAACCCGGGAGGTGGCAGTTGAGTGAGCTGAGATGAGGCCATGCATCCAGCTGGTGT
 GCAGAGAGCGAGACTCCATCTCAAAAAAAGAAAAAAGAAAAAAGAAAAAATGAAAAACATCC
 TCATGGCCCAAAAATAAGGTCTAATTTCAATAAATTTATAGTACATTAATGTAATTAATATTA
 CATGCCACTAAAAAGAATAAGGTAGCTGATATTTCCCTGGTATGAAAAAACATATTAATAT
 GTTATAAATCTAGGTTGGTGCAAAACTAATTTGGTGGTTTGGCATGAAATGGCATTGAA
 ATAAAAGTGTAAAGAAATCTATACCAGATGTAGTAACAGTGGTTTGGGCTGGGAGGTGGA
 TTAACGGGAGCAATTTGATTTCTATGTTGTATTTCTATAATGTTGAATGTTTGAATGTGA
 ATCTGATTTCTTTTATAGTAGAAAAAATAAAGATAGTTTTTACAGCCT

FIGURE 34

MRLIRNIYIFCSIVMTAEGDAPELPEERELMTNCSNMSLRKVPADLT PATTTLDLSYNLLFQ
LQSSDFHSVSKLRVLILCHNRIQQDLKTFEFNKELRYLDLSNNRLKSVTWYLLAGLRYLDL
SFNDFDTPICEEAGNMSHLEILGLSGAKIQKSDFQKIAHLHLNTVFLGFRTPHYEEGSLP
ILNTTKLHIVLPMDTNFWVLLRDGIKTSKILEMTNIDGKSQFVSYEMQRNLSLENAKTSVLL
LNKVDLLWDDFLILQFVWHTSVEHFQIRNVTFGGKAYLDHNSFDYSNTVMRTIKLEHVHFR
VFYIQQDKIYLLLT KMDIENLTISNAQMPHMLFPNYPTKFQYLN FANNILTDELFKRTIQLP
HLKTLILNGNKLETLSLVSCFANNTPLEHLDLSQNLQHKNDENC SWPETVVNMNLSYNKLS
DSVFRCLPKSIQILD LNNNQIQTPKETIHLMALRELNIAFNFLTDLP GCSHF SRLSVLNIE
MNFILSPSLDFVQSCQEVKTLNAGRNPFRCTCELKNFIQLETYSEVMMVGWSDSYTCEYPLN
LRGTRLKD VHLHELSCNTALLIVTIVVIMLVGLAVFCCLHFDLPWYLRMLGQCTQTWHRV
RKTTEQLKRNVRFHAFISYSEHDSLWVKNELIPNLEKEDGSILICLYESYFDPGKSISENI
VSFIEKSYKSIFVLPNPFVQNEWCHYEFYFAHNNLFHENS DHIILILLEPIPFYCIPTRYHK
LKALLEKKAYLEWPKDRRKCGLFWANLRAAINVNVLATREMYELQTFTELNEESRGSTISLM
RTDCL

FIGURE 35

FIGURE 36

MSRPGTATPALALVLLAVTLAGVGAQGALEDPDYYGQEIWSREPYARPEPELETFSPLP
AGPGEWERRPQEP RPPK RATKPKKAPKREKSAPEPPPGKHSNKKVMRTKSSEKAANDDHS
VRVAREDVRESCPPLGLETLKITDFQLHASTVKRYGLGAHRGRNLNIQAGINENDFYDGAWCA
GRNDLQQWIEVDARRLTRFTGVITQGRNSLWLSDWVTSYKVMVSNDSHTWVTVKNGSGDMIF
EGNSEKEIPVLNELPVPVMVARYIRINPQSWFDNGSICMRMEILGCPLPDNNYYHRRNEMTT
TDDLDFKHHNYKEMRQLMKVNVNEMCPNITRIYNIGKSHQGLKLYAVEISDHPGEHEVGEPEF
HYIAGAHGNEVLGRELLLLLVQFVCQEYLARNARIVHLVEETRIHVLP SLNPDGYEKAYEGG
SELGGWSLGRWTHDGDIDINNFPDLNLTLLWEAEDRQNVPRKVPNHYYIAIPEWFLSENATVAA
ETRAVIANMEKIPFVLGGNLQGGELVVAYPYDLVRSPWKTQEHTPTPDDHVFRWLAYSYST
HRLMTDARRRVCHTEDFQKEEGTVNGASWHTVAGSLNDFSYLHTNCFELSIYVGCDKYPHES
QLPEEWENNRESLIVFMEQVHRGIKGLVRDSHGKGPINAIISVEGINHDIRTANDGDYWRLL
NPGEYVVTAKAEGFTASTKNCMVGYDMGATRCDFTL SKTNMARIREIMEKFGKQPVSLPARR
LKLGRKRKRRQG

FIGURE 37

CTAAGAGGACAAAGATGAGGCCGGGCTCTCATTCTCTAGCCCTCTGTCTCTCTTGGCCAAGCTGCAGGGG
 ATTTGGGGGATGTGGGACCTCCAATTCCCAGCCCCGGCTTCAGCTCTTTCCAGGTGTTGACTCCAGCTCCAGC
 TTCAGCTCCAGCTCCAGCTCCGGCTCCAGCTCCAGCCGACGCTTAGGCAGGGGAGGTTCTGTGCCAGTTGTT
 TTCATATTTCCAGCGCTCCGTGGATGACCGTGGGACCTGCCAGTGTCTGTGTTCCCTGCCAGACACCACTTTCC
 CCGTGGACAGAGTGGAAACGCTTGAATTCACAGCTCATGTTCTTTCTCAGAAGTTTGAGAAAGAACTCTAA
 GTGAGGGAATATGTCCAATTAATTAGTGTCTATGAAAGAACTGTTAAACCTTAACCTGTCCGAATTGACATCAT
 GGAAGAGGATACCAATTTCTTACACTGAACCTGGACTTCGAGCTGATCAAGGTGAGAATGAAGGAGATGAAAGAA
 ATGACTCTCTTGGTAGAGAGCTTGAGACACTAGACAAAACCAATGTCCTTGCCATTGCCGAGAAATCCCTGCC
 TCTGAAGACCAAGCTGAAAGAGTGTGAGGCCCTCTAAAGATCAAAACACCCCTGTGCTCCACCTCCCTCCACTC
 CAGGGAGCTGTGGTCATGTTGGTGTGGTGAACATCAGCAAAACCGCTCTGTGGTTCCAGCTCAACTGGAGAGGGTTT
 TCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTCCACAGCATCCAAACAAGGACTGTATTGGGTGGCGCC
 ATTTGAATACAGATGGGAGACTGTTGGATATTATAGACTGTACAACACACTGGATGATTGCTATTGTATATAA
 ATGCTCGAGAGTTGCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAAC
 ATGTACAACACCGGGAATATTGCCAGAGTTAACCTGACCACCAACACGATTGCTGTGACTCAAACTCTCCCTAA
 TGCTGCTATAATAACCGCTTTTCATATGCTAATGTTGCTTGGCAAGATATTGACTTTGCTGTGGATGAGAATG
 GATTGTGGGTTATTATTCAACTGAAGCCAGCACTGGTAACATGGTGATTAGTAAACTCAATGACACCACTTT
 CAGGTGCTAAACACTTGGTATACCAAGCAGTATAAACCATCTGCTTCTAACGCCTTCATGGGTATGTGGGGTTCT
 GTATGCCACCCGTACTATGAACACCAGAACAGAGAGATTTTTACTATTATGACACAAACAAGGAGGAGAGG
 GCAAACTAGACATTGTAATGCATAAGATGCAGGAAAAAGTCAGAGCATTTAACTATAACCCCTTTGACCAAGAAA
 CTTTATGCTATAACGATGGTTACCTTCTGAATTAATGATCTTTCTGCTTGCAGAAAGCCCAAGTAAAGCTGTTA
 GGAGTTAGGGTGAAGAGAGAAATGTTGTTGAAAAAATAGTCTTCCACTTACTTAGATATCTGCAGGGGGTGT
 CTAAGAGCTGTGTTCAATTTGCAGCAATGTTAGGTGCATAGTTCTACCACACTAGAGACTAGGACATTTGCT
 TGAATTTGGTGGATCTCTTTGGGAATCATCTGCTTCTCAGGCGCATTTTGATAAAGCTCTGTCTAGGGTGGGA
 TTGTCAAGGGCTCAGGGGCACTGTGGGCTTAGTGAAGCCTACTGTGAGGAGGCTTCACTAGAAGCCTTAAATTA
 CGAATTAAGAACTTAAACTCAGTATGGGCTCAGGGATTCTTTGTACAGGAATATTGCCAATGACTAGTCTC
 CTATCCATGTAGGCCCACTAATTCTTCCATGCTTGAAGAAACCTGGGGACTTGTAGGTAGATTAAATATCT
 GGAGCTCCTCGAGGGACCAAACTCCAATTTTTTTTCCCTCACTAGCACCTGGAATGATGCTTTGTATGTGG
 CAGATAAGTAAATTTGCCATGCTTATATATTCTACATCTGTAAGTGTGAGTTTTATGGAGAGAGGCTTTTT
 ATGCATTAAATTTGACATGGCAATAAATCCAGAAGGATCTGTAGATGAGGCACCTGCTTTTTTCTTTCTCTC
 ATTCTCCACCTTACTAAAGTCACTAGAATCTTCTACCTCATAACTTCTTCCAAAGGCAGCTCAGAAGATTAG
 AACAGACTTACTAACCAATTTCCACCCCAACCAACCCCTTCTACTGCCTACTTTAAAAAAATTAATAGTTTT
 CTATGGAAGCTGATCAAGATTAGAAAAATTAATTTTCTTAATTTTCAATTATGGACTTTTATTTACAGCTCTA
 AGACTATAGAAAAATCTATGTCAGTACAAAGCTGACAAAGCTGCTAGCACTTTATGTTATCAATAAAGACCTTGAGCATA
 TGTGCAACTTATAGTGTATCAGTTGTTGATGTAATTTTGCCCTTTGTTAAAGCCTGGAACCTTTGAAGAAAT
 GAAAAATTAATTTTTTTCTAGGACGAGCTATAGAAAAAGCTATTGAGAGTATCTACTAATCAGTGCAGTAGT
 TGAAGACCTTGCTGGTGTATGTGTGCTCTGTGCTTTTGAATGACTTTATCATCTAGTCTTTGTCTATTTT
 TCCCTTTGATGTTCAAGTCCATGCTATAGGATTGGCAGTTTAAGTGCTTTACTCCCCCTTTTAAAAATAATGAT
 TAAAAATGTGCTTTGAAAAAAGAAAAAAGAAAAAAGAAAAA

FIGURE 38

MRPGLSFLALLFFLGQAAGDLGDVGPPIPSPGFSSFPGVDSSSSSFSSSSSRSGSSSSSRSLGS
 GGSVSQFLFSNFTGSDVDRGTCQCSVSLPDTTFPVDRVERLEFTAHVLSQKFEKELSKVREYV
 QLISVYEKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGGSSEIVDQ
 LEVEIRNMTLLVEKLETLDKNNVLAIRREIVALKTLKECEASKDQNTFVVHPPPTPGSCGH
 GGVDNISKPSVVQLNWRGFSYLYGAWGRDYSPOHPNKGlyWVAPLNTDGRLLLEYRlyNTLD
 DLLLYINARELRITYGQSGTAVYNNNMVNMNTGNiARVNLTNTIAVTQTLpNAAYNNR
 FSYANVAWQDIDFAVDENGLWVIYSTEASTGNMVISKLNDDTLQVLNTWYTKQYKPSASNAF
 MFCGVLYATRTMNTREEIFYYYDTNTGKEGKLdivMHKMQEKVQSiNYNPFdqKLYVNDG
 YLLNYDLSVLQKpQ

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FIGURE 39

GCTCTGAAGACCAAGCTGAAAGAGTGTGAGGCCTCTAAAGATCAAACACCCCTGTCGTCCAC
CCTCCTCCCACCTCCAGGGAGCTGTGGTCATGGTGGTGTGGTGAACATCAGCAAACCGTCTGT
GGTTCAGCTCAACTGGAGAGGGTTTTCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTC
CCCAGCATCCAAACAAAGGNATGTATTGGNGGCGCCATTGAATACAGATGGGAGACTGTTG
GAGTATTATAGACTGTACAACCCACTGGATGATTTGCTATTGTATATAAATGCTCGAGAGTT
GCGGATCACCTATGGCCAAGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAACA
TGTACAACACCGGGNATATTGCCAGAGTTAACCTGACC



FIGURE 40

TCTCGCAGATAGTAAATAATCTCGGAAAGGCCGAGAAAGAGCTGTCTCCATCTTGTCTGTAT
 CCGCTGCTCTTGTGAGCTTGTGGAGATGGGGAGCGCTCCTGGGGCTGTGCTCCATGGCGAGCT
 GGTATACCATGTTTGTGTGGAGTGCCCGGTGTTTGCATGCCGATGCTGTCTAGTGGAAAC
 AACTCCACTGTAACTAGATGATCTATGCACTTTTCTGCTTGTGGAGTATGTGTAGCTTG
 TGTAAATGTGATACCAGGAATGGAAGAACAACTGAATAAGATTCTCGGATTTTGTGGAATG
 AGAAAGGGTGTCTCCCTTGTAACTATTTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTT
 GGTTTGGCTATGCTTCTATCTTCTCTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGA
 TCCTAGAGCTGCAGTGCACAAATGGATTTTGGTTCTTTAAATTTGCTGCAGCAATTGAATTA
 TTATTTGGGCAATTTCTTCATCCAGAAGGAACTTTACAACGTGTGTGGTTTTATGTAGGCATG
 GCAGGTGGCTTTGTTTCATCCTCATACAACTAGTCTTACTTATTTGATTTTGCACATTCATG
 GAAATGAATCGTGGGTTGAAAAAATGGAAGAAGGGAACTCGAGATGTTGGTATGCGACCTTGT
 TATCAGCTACAGCTCTGAATTATCTGCTGCTTTAGTTGCTATCGTCTGTTCTTTGTCTAC
 TACACTCATCCAGCCAGTTGTTTACAGAAACAAGGCGTTTCATCAGTGTCAACATGCTCCTCTG
 CGTTGGTCTCTGTAAATGTCTATACTGCCAAAAATCCAAGAATCACAAACCAGATCTGGTT
 TGTACAGTCTTCAGTAATTACAGTCTACACAATGTATTTGACATGGTCAGCTATGACCAAT
 GAACCAAGAAATTTGCAACCCCAAGTCTACTAAGCATAAATGGCTACAATACAACAAGCAC
 TGTCCCAAGGAAGGGCAGTCACTCCAGTGGTGGCATGCTCAAGGAATATAGGACTAATTC
 TCTTTTTGTGTGTGATTTTTATCCAGCATCCGTACTTCAAACAATGAGTCAAGGTTAATAAA
 CTGACTCTAACAGTGAATGAATCTACATTAATAAGAAGTGGTGAGAGTAGAAGTATGGATC
 ACTGGAGGTATGGGACGATGTTCAACGAGCTGTAGATAATGAAAGGGATGGTGTCACTTACA
 GATATTCTTCCAGTTGGATTGTCATGCTTTTCTGGCTTCACTTTATATCATGATGACCTTACC
 AACTGGTCCAGGTATGAACCTCTCGTGAGATGAAAAGTCAGTGGACAGCTGTCTGGGTGAA
 AATCTCTCCAGTTGGATTGGCATCGTGCTGTATGTTTGGACACTCGTGGGCACTTGTGTC
 TTATAAATCGTGATTTTGACTGAGTGTAGTGAAGTTCCTAGCATGAAAGTCCCACTTTGATTATGTC
 TTACTTGAACACGTATTTCCAACTTTTGTAAAGTTGTGTATGTTTTGCTTCCCATTGAAC
 TTCTCCAGTGTCTGGCATGAATAGATTTTACTGCTGTGCTATTTGTTATTTTCTTACC
 GTGCATGATATGTGAAGTGAATGAATTTGCAGAGGAAAGTTTTATGAATGGTGATGAGT
 TAGTAAAGTGGCCATTTATTTGGGCTTATTTCTCTGCTCTATAGTTGTGAATGAAGAGTAAAA
 ACAAATTTGTTTGAATTTTAAAAATATATTAGACCTTAAGCTGTTTTAGCAAGCATTTAAA
 GCAAAATGTATGGTGCCTTTTGAATATTTGATGTGTGCTGGCAGGATACGCAAGAAAC
 ATGGTTTTATTTTAAAAATTTATAACAAGTCACTTAAATGCCAGTTGCTGAAAAATCTTATA
 AGGTTTTACCTTGATACGGAAATTTACACAGGTAGGGAGTGTATAGTGGACAATAGTGTAGG
 TTATGGATGGAGGTGTGCTGTAATAATGAATAACGAGTAAATAATCTTACTGGGTAGAGA
 TGGCCTTTGCCAACAAAGTGAACCTGTTTTGGTTGTTTTAACTCATGAAGTATGGGTTTCAGT
 GGAAATGTTTGGAACTCTGAAGGATTTAGACAAGGTTTTGAAAAGGATAAATCATGGGTTAGA
 AGGAAGTGTTTGAAAGTCACTTTGAAAGTGTAGTTTGGGCCCCAGCCAGGTAGCTCACCCTT
 GGTAAATCCCAGCACTTTGGGAGCTTAAAGTGGGTAGATTACTTGAAGCCAGGAATTCAGACCA
 GCTTGGCAGATGGTGAACCTGTCTATAAAAAATAACTGGCTTTGAGCATATGCTTGGTGT
 CAGCATGAGAGCTAGTGAAGATTGCTGAGCCAGAGCCAAAGGTGCGAGTGGCAAGTCA
 CGTCACTGCACTCTAGCTGGCAGAGTAGGCCAAAAAATATATATATATGAAATCAAGG
 AGGCAAAAATTTGACAGGGAAGGAAGTAACGCAAAACCACTAGGCTTTAGTAGGTACTTAT
 ATAAATCTAGTCAGTCTCTCATTTTAAAAAATGAAGACACTGAAATACAGACTTAAATTA
 GTCAGATAGCTAATTAGGAAATTTCAAGTTGGCCAATAATAGCATTCTCTCTGACATTTAA
 AAATAATTTCTATCAAATACATGCATATTGATTTACACCTCATACTGTGATAATTAATGT
 GATGTGGATTGCTGGTCTCAGCATGACCATAAACAGGTGAGAAGATGATGGAATGTTTT
 AGAATAAACCTCTGCTTATAGTATATACACAGTTCAAAGAGTGTTTAAATGCTTTTGTAT
 TTACTGCCATGTAATTGAAATATATAGATTGATTTGTAACCTTCAACCTGAAATCAAGCAGT
 ATGAGAGTTTAGTTATTTTATGTGTGCTAGTGTCTAATGAAGCTTTTAAATCTCAAAAT
 TCTTCTTAAAAAATTTTAAATGTGAATGGAATATAACAAATCAGCTTAATCCCCAACCC
 TTATCTGTGTGAGACATTTGATTTCCACAATTTTGAATGGCTGTGTTTTACCTCTAAATAA
 ATGAATTCAGAGAAAAA

FIGURE 41

MGSVLGLCSMASWIPCLCGSAPCLLCRCCPSGNNSTVTRLIYALFLLVGVCVACVMLIPGME
EQLNKIPGFCENEKGVVPCNILVGKAVYRLCFGLAMFYLLSLLMIKVKSSSDPRAAVHNG
FWFFKFAAAIAIIIGAFFIPEGTFTTVWFYVGMAGAFCFILIQVLVLLIDFAHSWNESWVEKM
EEGNSRCWYAALLSATALNYLLSLVAIVLFFVYYTHPASCSENKAFISVNMMLLCVGASVMSI
LPKIQESQPRSGLLQSSVITVYTMYLTSAMTNEPETNCNPSLLSIIGYNTTSTVPKEGQSV
QWWHAQGIIGLILFLLCVFYSSIRTSNNSQVNKLTLTSDESTLIEDGGARSDGSLEDGDDVH
RAVDNERDGVITYSYFFHFMLFLASLYIMMTLTNWSRYEPSREMKSQWTAVVWKISSWIGI
VLYVWTLVAPLVLTNRDFD

FIGURE 42

GCGAGAAAGAAGCTGTCTCCATCTTGTCTGTATCCCGCTGCTTCTTGNGACGTTGTGGAGAT
GGGGAGCGTCCCTGGGGCTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCC
CCGTGTTTTGCTATGCCGATGCTGTCCTAGTGGAAACAANTCCACTGTAAC TAGATTGATCTA
TGCAC TTTTCTTGCTTGTTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAG
AACAACTGAATAAGATTCTTGGATTTTGTGAGAATGAGAAAGGTGTTGTCCCTTGTAACATT
TTGGTTGGCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGGCTATGTTCTATCTTCTTCT
CTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGAT
TTTGGTTCTTTAAATTGCTGCAGCAATTGCAATTATTATTGGGGC

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FIGURE 43

GTTATTGTGAACTTTGTGGAGATGGGAGGTCNTGGGGCTGTGTTCCATGGCGAGCTGGATAC
CANGTTTGTGTGGAAGTGCCCCGTGTTTGNATGCCGATGCTGTCCTAGTGGAAACAANTCC
ACTGTAATTAGATTGATNTATGCACTTTTNTTGCTTGTTGGAGTANGTGTAGCTTGTGTAAT
GTTGATACCAGGAATGGAAGAACAACGAATAAGATTCCTGGATTTTGTGAGAATGAGAAAG
GTGTTGTCCCTTGTAACATTTTGGTTGGCTATAAAGCTGTATATNGTTTGTGCTTTGGTTTG
GCTANGTTCTATNTCTTCTCTTTACTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAG
AGCTGCAGTGCACAATGGATTTTGGTTTTTTAAATTGCTGCAGCAATTGCAATTATTATTG
GGGC

FIGURE 44

AAGAAGCTGTCTCCATCTTGTCTGTATCCGCTGCTCTTGTGAACGTTNTGGAGATGGGGAGC
GTCCTTGGGGTTGTGCTCCATGGCGAGCTGGATACCATGTTTGTGTGGAAGTGCCCCGTGT
TGCTATGCCGATGCTGTCTAGTGGAAACAACCTCCACTGTAAC TAGATTGATCTATGCACTT
TTCTTGCTTGTTGGAGTATGTGTAGCTTGTGTAATGTTGATACCAGGAATGGAAGAACAAC
GAATAAGATTCTGGATTTTGTGAGAATGAGAAAGGTGTTGCTCCCTTGTAACATTTTGGTTG
GCTATAAAGCTGTATATCGTTTGTGCTTTGGTTTGCTATGTTCTATCTTCTCTCTCTTA
CTAATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGCACAATGGATTTTGGTT
CTTTAAATTGCTGCAGCAATTGCAATTATTATTGGGGC

FIGURE 45

GCTGTCCTTAGTGAAACAANTCCAACCTGTAACCTGGATTGATCTATGCACCTTTTCCTTG
CTTGTGAGATATGTGTAGCTTTGTGAATGTTGTGCCAGGATTGGANGAACAACTGAATA
AGATTCTGGATTTTTGTGAGAAAGGTGTTGTCCCTTGTAACATTTTTGGTTGGC
TATAAAGCTGTATATCGTTGTGCTTTGGTTGGCTATGTTCTATCTTCTCTCTTTACT
AATGATCAAAGTGAAGAGTAGCAGTGATCCTAGAGCTGCAGTGACAAATGGATTTTTGGTTCT
TTAAATTTGCTGCAGCAATTGCAATTATTATTGGGGCATTCTTCATCCAGAAGGAACTTT
ACAACTGTGTGGTTTTATGTAGGCATGGCAGGTGCCTTTTGTTCATCCTCATACAAC TAGT
CTTACTTATTGATTTTGCACATTCATGGAATGAATCGTGGGTGAAAAATGGAAGAAGGGA
ACTCGAGATGTTGGTATGCAGCCTTGTTATCAGCTACAGCTCTGAATTATCTGCTGTCTTTA
GTTGCTATCGTCTGTTCTTTGTCTACTACACTCATCCAGCCAGTTGTTGAGAAAACAAGGC
GTTTCATCAGTGTCACATGCTCCTCTGCGTTGGTGCCTTCTGTAATG

FIGURE 46

CTCGGGCGCGCAGGAGCTCGGTTGGCCCTGCGATTGAGCTGCGGGTCGCGGCGCGGCGCGGCTCTCCAAT
 GGCAAATGTGTGTGGCTGGAGCGAGCGCGAGGCTTTCGGCAAAGGCAGTGCAGTGTTCGAGACCGGGGCGAG
 TCTCTGTGAAGACAGATAAAAGAAACATTTATTAACGTGTCAATTACGAGGGGACGCCGCGCGGGGCTGTGCGC
 ACTCCCGCGGAACTTTGGCTCCCTCCAGCTCCGAGAGGAGGAGAAGAAAGCGGAAAGGAGGACAGATCAC
 GCTGTTTCCAGCGCAAGTGGACCTCATCGATGGCCCTCTGAATTTATCAGNATTTTGATTTATTAGCGATGCC
 CTTCTGTTTGTGTGTACGACACACACAGCTGCACACAGGCTCTGGCTCGCTTCCTCCCTGTTTCCAGCTCC
 TGGGCGAATCCACATCTGTTTCACTCTCCCGCGAGCGCAGCAGAGCGAGATGTGTGSAATCTGCGAGTG
 AAGAGGGACGAGGGAAGAAACAAAGCCACAGACGCACTTGAGACTCCGCGATCCCAAAGAGCAACAGAT
 CAGCAAAAAAGAAAGATGGGCCCCCGAGCCTCGTGCTGTGCTGTGCTGTCGCGCACTGTCTCTCCGCTGGG
 TGGAGCTCGGCTTCTGTGCGACACCGCCTGAAAGGCAGGTTTCAGAGGGACCGCAGGAACATCCGCCCA
 ACATCATCTCGTGTGACGAGGACACAGGATGTGGAGCTGGGTTCCATGCGAGTGATGAACAGACCCGGGCG
 ATCATGGAGCAGGGCGGGGCGCATTCATCAACGCTTCGTGACCACACCATGTGCTGCCCTCAGCGCTCTCT
 CATCTCACTGGCAAGTACGTCCACAACCAACACACTACACCAACAATGAGAAGTGTCTCCGCTCCTGCTGGC
 AGGCACAGCAGGAGAGCCGACCTTTGCGGTGTACCTCAATAGCATGGCTACCGGACAGCTTTCTCCGGGAAG
 TATCTTAATGAATACAACGGCTCTACGTGCCACCCGGCTGGAAGAGTGGTGGGACTCCTTAAAAAATCCCG
 CTTTATAACTACACGCTGTGTGCGGACGGGTTGAAAGAGAAGCAGCGCTCCGACTACTCCAAGGATTACCTCA
 CAGACCTCATCAACCAATGACAGCGCTGAGCTTCTTCGCGAGTCCAAGAAGATGTACCCGCAAGCGGACTCTCT
 ATGCTCATCAGCCATGACGCCCCCAGCGGCTGAGGATTCAGCCCCAATATTCACGCTTTCTCCAAACGC
 ATCTCAGCAGCTACAGCCGAGTACAATACGCGCCCAACCCGAGCAACACTGGATCATGGCTTACAGGGGCG
 CCTGAAGCCATCCACATCGAATTCACCAACATCTCCAGCGGAAAGCGCTTGACAGCCCTCATGTCCGGTGAAC
 GAGTCACTGGAGAGGATTTACACATGCTGGTTGAGACGGGCGAGCTGGACAACAGCTACATCGTATACACCGC
 CGACCCGGTTCACACATCGGCGAGTTTGGCCTGGTGAAGGGAAATCCATGCGCATATGATGTTGACATCAGG
 TCCGCTTCTACGTAGGGGGCCCCAAGCTGGAAGCGGCTGTCTGAATCCCCACATCTCTCAACATGACCTG
 CGCCCTACCATCTTGGACATTCAGGGCTGGACATACCTGCGGATATGGACGGGAATCCATCCTCAAGCTGCT
 GGACCGGAGCGGCGGCTGAATCGGTTTCACTTGAAGAAAGATGAGGTTCTGGCGGAGTCTCTTCTGGTGG
 ACAGAGCAAGCTGCTACACAAGAGAGACAATGACAAGTGGAGCGCCGAGGAGGAACTTTCTGCCAAAGTAC
 CAGCGTGTGAAGACCTGTGTGAGCTGCTGAGTACAGACGGCGTGTGAGCAGCTGGGACAGAAAGTGGCAGTG
 GTGTGAGGAGCGCCAGCGGAAAGCTGAACTGCATAAGTGCRAAGGGCCCATGCGGCTGGGCGGACGACAGGCC
 TCTCCAACTCTGCGCCAAGTACTACGGGCGAGGCGAGCGAGGCTGCACTGTGACAGCGGGGACATACAAGCT
 AGCCTGCGCGCGCCGCGGAAAAAATCTTCAAGAAGAAATACAAGGCCAGCTATGTGCGCAGTGTCTCCATCG
 CTCAGTGGCCATCGAGGTGGACGGCAGGGTTACACAGTAGGCTGGGTGATGCGCGCCAGCCCGAAACCTCA
 CAAAGCGGCACTGGCCAGGGGCCCCGAGGACCAAGATGACAAGGATGTTGGGGACTCATGTGGCACTGGAGGC
 CTTCCGCACTACTCAGCGCCCAACCCATTAAATGACACATCGGTGCTACATCTAGAGAACGACAGATCCA
 GTGTGACCTGGACCTGTACAAATCCCTGCAGGCTGGAAGAACCAAGCTGCACATGCACACAGAGATTGAAA
 CCGTGCAGACAAATTAAGAAGCTGAGGGAAGTCCGAGGTCACTTGAAGAAAGCGGCGGACAGAAATGTGAC
 GTGCACAAATCAGCTACCAACCCAGCACAAGGCCGCTCAGCAGCAGAGGCTCCAGTCTGCATCTTTCTGAC
 GAAGGCGCTGCARAGAGAGGACAAGTGTGGCTTTGGCGGAGCAGAAAGCCAGAGAAATCTCCGAGAGCTGC
 TCAAGCGCTGCAGACACAGCAGCATGCGAGCATGCCAGGCTCAGCTGTCTCCAGCAGACCCAGCATCGG
 CAGACGGCGCTTTCTGGACAGCTGGGGCTTTCTGTGCTGCACAGCGCCAAACATACACGATCTGGTGCAT
 GAGGACCATCAATGAGACTCACAAATTTCCCTCTTCTGTGAATTTGCAATGGCTTCTAGAGTACTTTGATCTCA
 ACAGACCCCTTACCAGCTGATGAATGAGTGAACACACTGGACAGGATGTCTCTCAACAGCTACAGTACAG
 CTCATGAGCTGAGGAGCTGCAAGGTTACAGACAGTGTAAACCCCGGACTGAAACATGGACTGATGGAG
 AAGCTATGAGCAATACAGGCAATTTCAAGCTGAAAGTGGCCAGCAATGAAGAGCCTTCTCCAAATCACTGG
 GACAATCTGGGAAGGCTGGGAAGTGTAAAGAAACACAGAGGTGGACCTCCAAAGACATAGAGGCTCACTGA
 CTGCACAGCAATGAAAAACCATGTGGGTGATTTGCAGCAGCTGTGCTATTTGGCAGGAGCCTGAGAAAGC
 AAGCAGCACTCTCATGTCAACATGACAGATTTCTGGAGGATAACCCAGGAGCAGAGATTAATCCAGAGATCC
 ATTTTGGCCCTGTTTGTGTTGATTTATACCTCACCAGTGCACAAATGCACTCTTTTGTATCAAAAGTCT
 ACCACTAACCTCCCCAGAGCTCACAAAGGAAACCGAGAGAGCGAGCGAGGAGAGATTTCTTGAAATTTCT
 TCCAAGGGCGAAAGTCAATGGAAATTTTAAATCATAGGGGAAAGCAAGTCTCTGTTTCAATCTCTTATTTCT
 TGTGTTGTCAAAAGAGGAACTAAGAGCAGGACAGAGGCAAGCTGGAGAGGCTGAAACAGTGCAGAGAGT
 TTTGCAATGAGTCAGTACACAAAAGAGATGACATTTACCTAGCATATAACCCCTGTTGCTCTGAAGAAA
 CTGCTTCTATTGTATATATGTACTATTTACATGTAATCAACATGGGAATTTTGAAGGAACCTAATAAGAAAT
 CCCAATTTTCAGAGTGTGTGCTCAATAAACGCTGTGGCCAGTGTAAAAGAAA

FIGURE 47

MGPPSLVLCLLSATVFSLLGGSSAFLSHHRLKGRFQDRRNIRPNIIILVLTDDQDVELGSMQ
VMNKTRRIMEQGGAHFINAFVTTPMCPCSRSSILTGKYVHNHNTYTNNENCSSPSWQAQHE
RTFAVYLNSTGYRTAFFGKYLNEYNGSYVPPGWKEWVGLLKNSRFYNYTLCRNGVKEKHGSD
YSKDYLTLITNDSVSFFRTSKKMYPHRPVLMVISHAAPHGPEDSAPQYSRLFPNASQHITP
SYNYAPNPKHWIMRYTGPMKPIHMEFTNMLQRKRLQTLMSVDDSMETIYNMLVETGELDNT
YIVYTADHGYHIGQFGLVKGKSMPIYEFDIRVPPFYVRGPNVEAGCLNPHIVLNLIDLAPTILDI
AGLDIPADMDGKSILKLLDTERPVMRFLKMKMRVWRDSFLVERGKLLHKRDNDKVDAQEEN
FLPKYQVRVKDLCQRAEYQTACEQLGQKWQCVEDATGKLLHKCKGPMRLGGSRALSNLVPKY
YGGGSEACTCDSGDYKLSLAGRRKKLFKKKYKASYVRSRSIRSVAIEVDGRVYHVGLGDAQ
PRNLTKRHWPGAPEDQDDKGGDFSGTGGLPDYSAANPIKVTHRCYILENDTVQCCLDLKYS
LQAWKDHKLHIHIEITLQNKIKNLREVRGHLKKRP EECDCCHKISYHTQHKGRLKHGSSSL
HPFRKGLQEKDKVWLLREQKRKKLRLKLLKRLQNNDTCSMPGLTCFTHDNQHWQTAPFWTLG
EFCACTSANNNTYWCMTINETHNLFCEFATGFLEYFDLNTDPYQLMNAVNTLDRDVLNQL
HVQLMELRSCKGYKQCNPRTRNMDLDGGSYEQYRQFQRRKWPEMKRPSSKSLGQLWEGWEG

AACAAAGTTTCAGTGACTGAGAGGGCTGAGCGGAGGCTGCTGAAGGGGAGAAAGGAGTGAGGA
 GCTGCTGGGCAGAGAGGGACTGTCCGGCTCCACAGTCGCTGGGCCCTCTGGGGAGCACAGCCC
 TCGTGGGATGGATCACAGGTGCTGCTGTGGCGGTCTGCTGCTGCTGCTGCTGCTGGCCACC
 TGCCTTTTCCACGGACGGCAGGACTGTGACGTGGAGAGGAACCGTACAGCTGCAGGGGGAAA
 CCGAGTCCGCCGGGCCAGCCTTGCCCTTCCGGCGGCGGGGCCACCTGGGAATCTTTACC
 ATCACCGTCATCTGGCCAGTATCTCATGTGCCGAATGTGGGCCTCCACCACCACCACCAC
 CCCGCCACACCCTCACCACCTCCACCACCACCACCACCCACCGCCACCATCCCCGCCA
 CGCTCGCTGAGGCTGTGCTGCGCGGTGCCTGTGGACAGCAGCTGCCCTGCCCTCCCATCTG
 TTCCAGGACAAGTGGACCCCATGTTTCCATGTGGAAGGATGCATCTCTGGGGTGAACGAGG
 GGAACAATAGACTGGGGCTTGCTCCAGCTGCATTGTCATGGCATGCCCCAGTGTAATATGGC
 AGCAGAGAATGGAGGAACACTGGGTCTGCAGTGCTGAAGGGTTTGGGGAGTGGAGAGCAAGG
 GTGCTCTTTTCGGGGCTGGACAGCCGCTTTGTGACAGTGACTCCCAGTGAGCCCCAGAAATG
 ACAAGCGTGTCTTGGCAGAGCCAGCACACAAGTGGATGTGAAGTGCCCGCTTGCACCTCCT
 ATCATGGTGCTGCAGGCCTCTGGCGGGCAGGGCATGGGAGAGGCCCTTGAGAATGTCTTTT
 GTGTTGGAGAGGAGCATGTGAGGCTGCACAGCTCAATTCTCGTGCCTTAGTCCAAGAAAT
 AAAAAACCATAAGAGCTTTAAAAAAGAAAAA

MLGLLGSTALVGWITGA AVAVLLLLLLLATCLFHGRQDCDVERNRTAAGGNRVRAQPWPER
RRGHLGIFHHHRHPGHVSHVPNVGLHHHHHPRHTPHHLHHHHHPHRHHPRHAR

FIGURE 50

GCGGGCTGCTGAGCTGCCTTGAGGTGCAGTGTGGGGATCCAGAGCC**ATG**TCGGACCTGCTA
 CTACTGGGCTGATTGGGGCCCTGACTCTCTTACTGCTGCTGACGCTGCTGGCCTTTGCCGG
 GTACTCAGGGCTACTGGCTGGGGTGGAAAGTGAGTGCTGGGTACCCCCCATCCGCAACGTCA
 CTGTGGCCTACAAGTTCACATGGGGCTCTATGGTGAGACTGGCGGCTTTTCTACTGAGAGC
 TGCAGCATCTCTCCCAAGCTCCGCTCCATCGCTGTCTACTATGACAACCCCCACATGGTGCC
 CCTGATAAGTGCCGATGTGCCGTGGGCAGCATCCTGAGTGAAGGTGAGGAATCGCCCTCCC
 CTGAGCTCATCGACCTCTACCAGAAAATTTGGCTTCAAGGTGTTCTCCTTCCCGGCACCCAGC
 CATGTGGTGACAGCCACCTTCCCCTACACCACCATTCTGTCCATCTGGCTGGCTACCCGCCG
 TGTCCATCCTGCCTTGACACCTACATCAAGGAGCGGAAGCTGTGTGCCTATCCTCGGCTGG
 AGATCTACCAGGAAGACCAGATCCATTTTCATGTGCCACTGGCACGGCAGGGAGACTTCTAT
 GTGCCTGAGATGAAGGAGACAGAGTGGAATGGCGGGGGCTTGTGGAGGCCATTGACACCCA
 GGTGGATGGCAGAGAGCTGACACAATGAGTGACACGAGTTCTGTAAGCTTGGAAAGTGAGCC
 CTGGCAGCCGGGAGACTTCAGCTGCCACACTGTCACCTGGGGCGAGCAGCCGTGGCTGGGAT
 GACGGTGACACCCGACGCAGCACAGCTACAGCGAGTCAGGTGCCAGCGGCTCCTCTTTTGA
 GGAGCTGGACTTGGAGGGCGAGGGGCCCTTAGGGGAGTCACGGCTGGACCTTGGGACTGAGC
 CCCTGGGGACTACCAAGTGGCTCTGGGAGCCCACTGCCCTGAGAAGGGCAAGGAG**TAA**CCC
 ATGGCCTGCACCCCTCCTGCAGTGCACTGCTGAGGAAGTGAGCAGACTCTCCAGCAGACTCT
 CCAGCCCTCTTCCTCCTTCCCTCTGGGGGAGGAGGGGTTCTGAGGGACCTGACTTCCCCTGC
 TCCAGGCCCTCTTGCTAAGCCTTCTCCTCACTGCCCTTTAGGCTCCCAGGGCCAGAGGAGCCA
 GGGACTATTTTCTGCACCAGCCCCAGGGCTGCCGCCCTGTGTGTCTTTTTTTCAGACTC
 ACAGTGAGCTTCCAGGACCCAGAATAAAGCCAATGATTTACTTGTTCACCTGGAAAAAAA
 AAAAAAAAAA

FIGURE 51

MSDLLLLGLIGGLTLLLLLTLLAFAGYSGLLAGVEVSAGSPPIRNVTVAYKFHMGlyGETGR
LFTESCSISPKLRsIAVYYDNPHMVPPDKRCrCAVGSILSEGEESpSPELIDLYQKFGFKVFS
FPAPSHVVTATFPYTTILSIWLATRrVHPALDTYIKERKLCAYPRLEIYQEDQIHfMCPLAR
QGDFYVPEMKETEWKWRGLVEAIDTQVDGTGADTMSDTSSVSLEVSpgSRETSaATLSPGAS
SRGWDDGDTRSEHSYSESgASGSSFEELDLEGEgPLGESRLDPGTEPLGTTKWLWEPTApEK
GKE

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FIGURE 52

CCGCGGGAACGCTGTCCTGGCTGCCGCCACCGAACAGCCTGTCCTGGTGCCCCGGCTCCCT
 GCCCCGCGCCAGT**CAT**GACCCCTGCGCCCCCTCACTCCTCCGCTCCATCTGCTGCTGCTGCT
 GCTGCTCAGTGCGGCGGTGTGCCGGGCTGAGGCTGGGCTCGAAACCGAAAGTCCCGTCCGGA
 CCTTCCAAGTGGAGACCCCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTTGGGA
 GACACGCTTACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCT
 GACCAGAGACCCCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGA
 GTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCCTTCTCACTTGGCCTAT
 GGAAAACGGGGATTTCCACCATCTGTCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCT
 GATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTTTGCCCTCTGGTAG
 GGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTTGGGTATCACCTATACAGAAAGGCCAAT
 AGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAGAA**TA**
ATAAATAATAAATTTTAAAAAACTTAAAAAAAAAAAAAAAAAAAA

FIGURE 53

MTLRPSLLPLHLLLLLLLLSAAVCRAEAGLETESPVRTLQVETLVEPPEPCAEPAAFQDGLHI
HYTGSLVDGRIIDTSLTRDPLVIELGQKQVIPGLEQSLLDMCVGEKRRRAIPSHLAYGKRGF
PPSVPADAVVQYDVELIALIRANYWLKLVKGILPLVGMAMVPALLGLIGYHLYRKANRPKVS
KKKLKEEKRNKSKK



FIGURE 54

CCCGGGAACGTGTTCTCTGGCTGCCGCACCCGAACAGCCTGTCCTGGTGCCCGGCTCCCTGC
CCCGCGCCAGTCATGACCTGCGCCCTCACTCCTCCCGCTCCATCTGCTGCTGCTGCTGC
TGCTCAGTGCGGCGGTGTGCCGGCTGAGGCTGGGCTCGAAACGAAAGTCCCGTCCGGACC
CTCCAAGTGAGACCTGGTGGAGCCCCAGAACCATGTGCCGAGCCCGCTGCTTTGGAGA
CACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACGTATTATTGACACCTCCCTGA
CCAGAGACCTCTGGTTATAGAACTTGGCCAAAAGCAGGTGATTCCAGGTCTGGAGCAGAGT
CTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATTCTCTCACTTGGCCTATGG
AAAACGGGGATTTCACCATCTGTCCAGCGGATGCAGTGGTGCAGTATGACGTGGAGCTGA
TTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGGGCATTTTGCCTCTGGTAGGG
ATGGCCATGGTGCCACCTCCTGGGCCTCATTTGGGTATCACCTATACAGAAAGGCCAATAGA
CCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAACAAGAGCAAAAAGAAATAATA
AATAATAAATTTTAAAAAACTTA

FIGURE 55

CCGAAAGTCCCGTCCGGACCCTCCAAGTGGAGACCCTGGTGGAGCCCCAGAACCATGTGCC
GAGCCCGCTGCTTTGGAGACACGCTTCACATACACTACACGGGAAGCTTGGTAGATGGACG
TATTATTGACACCTCCCTGACCAGAGACCCTCTGGTTATAGAAGCTTGGCCAAAAGCAGGTGA
TTCCAGGTCTGGAGCAGAGTCTTCTCGACATGTGTGTGGGAGAGAAGCGAAGGGCAATCATT
CCTTCTCACTTGGCCTATGGAAAACGGGGATTTCACCATCTGTCCCAGCGGATGCAGTGGT
GCAGTATGACGTGGAGCTGATTGCACTAATCCGAGCCAACTACTGGCTAAAGCTGGTGAAGG
GCATTTTGCCTCTGGTAGGGATGGCCATGGTGCCAGCCCTCCTGGGCCTCATTGGGTATCAC
CTATACAGAAAGGCCAATAGACCCAAAGTCTCCAAAAGAAGCTCAAGGAAGAGAAACGAAA
CAAGAGCAAAAAGAAATAATAAATAATAAATTTAAAAAACTTAAA

FIGURE 56

CTGCTGCATCCGGGTGTCTGGAGGCTGTGGCCGTTTGTGTTTCTTGGCTAAAAATCGGGGGAG
 TGAGGCGGGCCGGCGCGGCACACCGGGCTCCGGAACCACTGCACGACGGGGCTGGACTG
 ACCTGAAAAAAATGTCTGGATTTCTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGG
 GAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGAT
 TATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGATTTCAACCACTCATACCATGCCT
 GTGGTGTTATAGCAACCATAGCCTTCCTAATGATTAAATGCAGTATCGAATGGACAAGTCCGA
 GGTGATAGTTACAGTGAAGGTTGCTGCGGTCAAACAGGTGCTCGCATTGGCTTTTCGTTGG
 TTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTTATGTTG
 CTAAAGAAAAAGACATAGTATACCCTGGAATTGCTGTATTTTTCCAGAATGCCTTCATCTTT
 TTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGACTTATGGCAGTGAACACATCTGAT
 TTCCACAGCACAAACAGCCCTGCATGGGTTTGTGTTTTTTTACTGCTCACTCCCAACCTT
 TTGTAATGCCATTTTCTAACTTATTTCTGAGTGTAGTCTCAGCTTAAAGTGTGTAATACT
 AAAATCACGAGAACCTTAAACAACAACCAAAAATCTATTGTGGTATGCATTGATTAACTT
 ATAAAATGTTAGAGGAACTTTCACATGAATAATTTTTGTCAAATTTTATCATGGTATAATT
 TGTAAAAATAAAAAGAAATTACAAAAGAAATTATGGATTGTCAATGTAAGTATTTGTCATA
 TCTGAGGTCCAAAACCACAATGAAAGTGTCTGAAGATTAATGTGTTTATTCAAATGTGGT
 CTCTTCTGTGTCAAATGTTAAATGAAATATAAACATTTTTTAGTTTTTAAATATTCCGTGG
 TCAAAATTCCTCCTCACTATAATTGGTATTTACTTTTACCAAAAATCTGTGAACATGTAAT
 GTAACCTGGCTTTTGGAGGCTCCTCAAGGGGTGAGTGGACGTGTTGGAAGAGAGAAGCACCAT
 GGTCCAGCCACCAGGCTCCCTGTGTCCCTTCCATGGGAAGGTCTCCGCTGTGCCTCTCATT
 CCAAGGCGAGGAAGATGTGACTCAGCCATGACACGTGGTTCTGGTGGGATGCACAGTCACTC
 CACATCCACCACTG

FIGURE 57

MSGFLEGLRCSECIDWGEKRNTIASIAAGVLFFTGWIIIDA AVIYPTMKDFNHSYHACGVI
ATIAFLMINAVSNGQVRGDSYSEGCLGQTGARIWLFVGFMLAFGSLIASMWILFGGYVAKER
DIVYPGIAVFFQNAFIFFGGLVFKFGRTEDLWQ

FIGURE 58

TTCTTGGCTAAAATCGGGGGAGTGAGGCGGGCCGGCGCGGACACCGGGCTCCGGAACC
ACTGCACGACGGGGCTGGACTGACCTGAAAAAAATGTCTGGATTTCTAGAGGGCTTGAGATG
CTCAGAATGCATTGACTGGGGGGAAAAGCGCAATACTATTGCTTCCATTGCTGCTGGTGTAC
TATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGTTATTTATCCCACCATGAAAGAT
TTCAACCACTCATACCATGCCTGTGGTGTTATAGCAACCATAGCCTTCCTAATGATTAATGC
AGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTTGTCTGGGTCAAACAGGTG
CTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGG
ATTCTTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTATACCTGGAATTGCTGTATT
TTCCAGAATGCCTTCATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGC

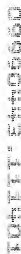


FIGURE 59

TGGACGGACCTGAAAAAATGTTTGGATTTNTAGAGGGNTTGAGATGTTTCAAGATGCATGAC
 TGGGGGAAAAGCGCAAATACTATTGCTTCCATTGCTGCTGGTGTANTATTTTTTACAGGCTG
 GTGGATTATCATAGATGCAGNTGTTATTTATCCCACCATGAAAGATTTCACCANTCATACC
 ATGCCTGTGGTGTTATAGCAACCATAGCCTTCNTAATGATTAATGCAGTATCGAATGGACAA
 GTCCGAGGTGATAGTTACAGTGAAGGTTGTTTGGGTCAAACAGGTGCTCGCATTTGGCCTTT
 CGTTGGTTTCATGTTGGCCTTTGGATCTCTGATTGCATCTATGTGGATTCTTTTTGGAGGTT
 ATGTTGCTAAAGAAAAAGACATAGTATACCCTGGAATTGNTGTATTTTTCCAGAATGCCTTC
 ATCTTTTTTGGAGGGCTGGTTTTTAAGTTTGGCCGCACTGAAGANTTATGGCAGTG

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FIGURE 60

GGACACCGGGTTCCGGACCAATGCANGACGGGGTGGANTGACCTGAAAAAATGTTTGGATT
TTTAGAGGGCTTGAGATGNTCAGAATGCATTGACTGGGGGAAAAGCGCAATANTATTGCTTT
CCATTGCTGCTGGTGTACTATTTTTTACAGGGTGGTGGATTATCATAGATGCAGCTGTTATT
TATCCCACCATGAAAGATTTNAACCACTCATACCATGCCTGTGGTGTATAGCAACCATAGC
CTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTT
GTTTGGGTCAAACAGGTGNTCGCATTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGGATTT
CTGATTGNATTCTATGCGGATTCTTCTTGGAGGTTATGTTGCTAAAGAAAAAGACATAGTAT
ACCCTGGAATTNCTNTATTTTTCCAGAATGCC

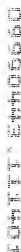


FIGURE 61

TAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGGAAAAGCGCAATANTATTGCTTCC
ATTGNTGNTGGTGTANTATTTTTTTACAGGCTGGTGGATTATNATAGATGCAGCTGTTATTT
ATCCCACCATGAAAGATTTNAACCANTCATACCATGCCTGTGGTGTATAGCAACCATAGCC
TTCCTAATGATTAATGCAGTATNGAATGGACAAGTCCGAGGTGATAGTTACAGTGAAGGTG
TTTGGGTCAAACAGGTGNTNGCATTGCGCTTTTNGTTGGTTTCATGTTGGCCTTTGGATCTN
TGATTGCATTTATGTGGATTNTTTTTGGAGGTTATGTTGCTAAAGNAAAAGACATAGTATAC
CCTGT

61/330

FIGURE 62

GGGAGGCTGTGNCCTTTTGTNTTGGCTAAAATCGGGGAGTGAGGCGGCCCGCGCGG
 CGNGACACCGGTTCCGGGAACCATTCACGACGGGGTGGACTGACCTGAAAAAATGTTTG
 GATTNTAGAGGGCTTGAGATGCTCAGAATGCATTGACTGGGGGAAAAGCGCAATACTATT
 GCTTCCATTGCTGCTGGTGTACTATTTTTTACAGGCTGGTGGATTATCATAGATGCAGCTGT
 TATTTATCCCACCATGAAAGATTCAACCACTCATACCATGCCTGTGGTGTTATAGCAACCA
 TAGCCTTCCTAATGATTAATGCAGTATCGAATGGACAAGTCCGAGGTGATAGTTACAGTGAA
 GGTGTCTGGGTCAAACAGGTGCTCGCATTTGGCTTTTCGTTGGTTTCATGTTGGCCTTTGG
 ATNTCTGATTGCATCTATGTGGATTCTTTTGGAGGTTATGTTGCTAAAGAAAAAGACATAG
 TATACCCTGGAATTGCTGTATTTTCCAGAATGCCTTCATNTTTTTTGGAGGGCTG

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FIGURE 63

CGACGCCGGCGTGA**ATG**TGGCTTCCGCTGGTGTGCTCCTGGCTGTGCTGCTGCTGGCCGTCC
TCTGCAAAAGTTTACTTGGGACTATTCTCTGGCAGCTCCCCGAATCCCTTTCTCCGAAGATGTC
AAACGCCGCCCGACGCCCTGGTAACTGACAAGGAGGCCAGGAAGAAGTTCTCAAACAAGC
TTTTTTCAGCCAAACCAAGTCCGGAGAAGCTGGATGTGGTGGTAATTTGGCAGTGGCTTTGGGG
GCCTGGCTGCAGCTGCAATTTCTAGCTAAAGCTGGCAAGCGAGTCTGGTGGTGGAAACAAT
ACCAAGGCGAGGGGGCTGCTGTCAATCTTTGGAAGAAAGTGGCCCTGAATTTGACACAGGAAT
CCATTACATTTGGGCGTATGGAAGAGGGCAGCATTTGGCCGTTTTATCTTGGACAGATCACTG
AAGGCCAGCTTGACGTGGGCTCCCTGTCTCTCTCTTTTACATCATGGTACTGGAAGGGCCCC
AATGGCCGAAAGGATACCCCATGTACAGTGGAGAGAAAAGCCTACATTCAGGGCCCTCAAGGA
GAAGTTTCCACAGGAGGAAGCTATCATTTGACAAGTATATAAAGCTGGTTAAGGTGGTATCCA
GTGGAGCCCCCTCATGCCATCTCTGTGAAATTCCTCCCATGGCCGTGGTTACAGTCCCTGGAC
AGGTGTGGGCTGCTGACTCGTTTCTCTCCATTCTCTCAAGCATCCACCCAGAGCCTGGCTGA
GGTCTGCAGCAGCTGGGGGCCCTCTCTGAGCTCCAGGCAGTACTAGCTACATCTTCCCCA
CTTACCGTGTCAACCCCAACCAAGTGCCTTTTCCATGCACGCCCTGCTGGTCAACCACTAC
ATGAAGAGAGGCTTTTATCCCGAGGGGGTTCCAGTGAAATTTGCCCTTCCACACCATCCCTGT
GATTACAGCGGGCTGGGGGCCCTGTCTTCAACAAGGCCACTGTGCAGAGTGTGTTGCTGGACT
CAGCTGGGAAAGCCTGTGGTGTCAAGTGAAGAAGGGGCATGAGCTGGTGAACATCTATTGC
CCCATCGTGGTTCTCAACAGCAGGACTGTTCAACACCTATGAACACCTACTGCCGGGGAACGC
CCGCTGCTGCCAGGTGTGAAGCAGCAACTGGGGACGGTGCGGCCCGGCTTAGGCATGACCT
CTGTTTTCATCTGCTGCGAGGCCACCAAGGAAGACCTGCATCTGCCCTCCACCAACTCATAT
TTTTACTATGACCGGACATGGACCAGGCGATGGAGCGTACGCTCTCCATGCCACGGGAAGA
GGCTGCGGAACACATCCCTTCTCTTCTTCTGCTTTCCCATCAGCCAAAGATCCGACCTGGG
AGGACGATTCCCAGCCGGTCCACCATGATCATGCTCATACCCATCGCTACGAGTGGTTTT
GAGGAGTGGCAGCGGAGCTGAAGGGAAAGCGGGCAGTGACTATGAGACCTTCAAAAACTC
TTTTGTGGAAGCTCTATGTCACTGGTCTTCAAAGTGTTCACAGCTGGAGGGGAAGGTGG
AGAGTGTGACTGCAGGATCCCCACTCACCAACCAAGTTCTATCTGGCTGCTCCCCGAGGTGCC
TGCTACGGGGTGACCATGACCTGGGGCGCTGCAACCTTGTGTGATGGCCCTCTTGGAGGGC
CCAGAGCCCCATCCCCAACCTCTATCTGACAGGCCAGGATATCTTACCTGTGGACTGTGTCG
GGGGCCTGCAAGGTGCCCTGCTGTGCAGCAGCGCCATCTTGAAGCGGAACTTGTACTCAGAC
CTTAAGAATCTTGATTCTAGGATCCGGGCACAGAAGAAAAAGAAAT**TAG**TTCATCAGGGAGG
AGTCAGAGGAATTTGCCCAATGGCTGGGGCATCTCCCTTGACTTACCCATAATGTCTTTCTG
CATTAGTTCCTTGCAGTATAAAGCACTCTAATTTGGTTCTGATGCCGTAAGAGAGGGCCTAG
TTTAAATCACAAATCCGAATCTGGGGCAATGGAATCACTGCTTCCAGCTGGGGCAGGTGAGA
TCTTTACGCCCTTTTATAACATGCCATCCCTACTAATAGGATATTGACTTGGATAGCTTGATG
TCTCATGACGAGCGGGCTGTGCATCCCTCACCATGGCTCCCTAAGTCACTGATCAAAAGCGA
ATATTCCATCTGTGGATAGAACCCTGGCAGTGTGTGCTCAGCTCAACCTGGTGGGTTCACTTC
TGTCTGAGGCTTCTGCTCTCATTCATTATTAGTGCTACGCTGCACAGTTCTACACTGTCAAGG
GAAAAGGGAGACTAATGAGGCTTAACTCAAAACCTGGGCGTGGTTTTGGTTGCCATTCCATA
GGTTTTGGAGAGTCTAGATCTCTTTTGTGCTGGGTTCACTGGCTCTTCAGGGGACAGGAAAT
GCCTGTGTCTGGCCAGTGTGGTTCTGGAGCTTTGGGGTAAACAGCAGGATCCATCAGTTAGTA
GGGTGATGTCAGATGATCATCAATTCATATGGAAGTCCCGGGTCTGTCTTCTTATCA
TCGGGGTGGCAGCTGGTTCTCAATGTGCCAGCAGGGACTCAGTACCTGAGCCCTCAATCAAGC
CTTATCCACCAATACACAGGGAAGGGTGTATGCAGGGAGGTGACATCAGGAGTCAAGGGCA
TGGACTGGTAAGATGAATACCTTTGCTGGGCTGAAGCAGGCTGCAGGGCATTCCAGCCAAAGGG
CACAGCAGGGACAGTGCAGGGAGGTGTGGGTAAAGGGAGGGAAGTCACTAGAAAAGGGGA
AAGCCACGGAATGTGTGTGAAGCCAGAAATGGCATTTGCAGTTAATTAGACAGTGTGAGGG
TTAGACAGGTAGGTGAATGCAGCTCAAGGTTTGGAAAAATGACTTTTCAAGTTATGCTCTTTG
GTATCAGACATACGAAGGTCCTTTGTAGTGTGTTAATGTAACATTAATAAATTTATTG
ATTCCATTGCTTTAAAAA

CGACGCCGGCGTGA

FIGURE 64

MWLPLVLLLAVLLLAVLCKVYLGLFSGSSPNPFSEDKVRPPAPLVTDKARKKVLKQAFSAN
 QVPEKLDVVVIGSGFGGLAAAAILAKAGKRVLVLEQHTKAGGCCHTFGKNLEFDTGIHYIG
 RMEEGSIGRFILDQITEGQLDWAPLSSPFDIMVLEGPNGRKEYPMYSGEKAYIQGLKEKFPQ
 EEAIIDKYIKLVKVSSGAPHAILLKFLPLPVVQLLDRCGLLTRFSFPLQASTQSLAEVLQQ
 LGASSELQAVLSYIFPTYGVTPNHSAFSMHALLVNHYMKGGFYPRGGSSEIAFHTIPVIQRA
 GGAVLTKATVQSVLLDSAGKACGVSVKKGHELVNIYCPVVSNAGLFNTYEHLLPGNARCLP
 GVKQQLGTVRPGLMTSVFICLRGTEDLHLPSTNYVYDYDTMDQAMERYVSMFREEAAEH
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FIGURE 66

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FIGURE 67

CTTCCCAGCCCTGTGCCCCAAAGCACCTGGAGCATATAGCCTTGCAGAACTTCTACTTGCCT
GCCTCCCTGCCTCTGGCCATGGCCTGCCGGTGCCCTCAGCTTCCTTCTGATGGGGACCTTCCT
GTCAGTTTCCCAGACAGTCTGGCCCAGCTGGATGCACTGCTGGTCTTCCCAGGCCAAGTGG
CTCAACTCTCCTGCACGCTCAGCCCCAGCACGTCAACATCAGGGACTACGGTGTGTCTGG
TACCAGCAGCGGGCAGGCAGTGGCCCTCGATATCTCCTCTACTACCGCTCGGAGGAGGATCA
CCACCGGCCTGCTGACATCCCGATCGATTCTCGGCAGCCAAGGATGAGGCCACAATGCCT
GTGTCTCACCATTAGTCCCGTGACGCTGAAGACGACGCGGATTACTACTGCTCTGTTGGC
TACGGCTTTAGTCCCTAGGGGTGGGTGTGAGATGGGTGCCTCCCCTCTGCCTCCCATTCT
GCCCCTGACCTTGGGTCCCTTTTAAACTTTCTCTGAGCCTTGCTTCCCCTCTGTAAATGGG
TTAATAATATTCAACATGTCAACAAC

FIGURE 68

MACRCLSFLMGTFLSVSQTVLAQLDALLVFPQVAQLSCTLSPQHVTIRDYGVSWYQQRAG
SAPRYLLYYRSEEDHHRPADI PDRFSAAKDEAHNACVLTISPVPEDDADYYCSVGYGFSF

68/330

FIGURE 69

GCGGCCCCGCGCCGAGACCGGGCCCGGGGGCGCGGGCGCGGGATGCGGCGCCCGGGGCGG
 CGATGACCGCGGAGCGACGCGCGGGCGCGGCCCTGACCCCGCGCGCCCGCCGTGAGCCCC
 CCGCGCGAGGTGCTCCGAGAGCGGATGACGCGCGAGCCCTGTTGCTGCTCTGCTGCCCG
 CGGTGCTGCTGCGGGGCGTCTCCACCGCGCGCGCGCGCGGAGGCCCCCAAGATGGCGGAC
 AAGTGGTGTCCACCGGACAGTGGCCCGGCTGGGCGCACTGTGCGGCTGCACTGCGCAGTGGA
 GGGGAGACCGCGCGCGCTGACCATGTGGACCAAGGATGGCCGCACTTCCACAGCGGGCTGGA
 GCGGCTTCCGCGTGTGCGCGAGGGGCTGAAGGTGAAGCAGGTGGAGCGGGAGGATGCGCGG
 GTGATACGTGTGCAAGGCGACCAACGGCTTGGCGAGCCTGAGCGTCAACTACACCTCGTGT
 GCTGGATGACATGATGCCAGGAGAGGAGCCTGGGCGCGCAAGCTCCTCTGGGGGTCAAG
 AGGACCCCGCAGGACGAGTGGGCGACGACCGCGCTTCAACAGCCCTCCAAGATGAGGCGC
 CCGGTGATCGCAGCGCGCGTGGGTAGCTCCGTGCGGCTCAAGTCCGTGGCCAGCGGGCACCC
 TCGGCCCCGACATCGATGGATGAAGGACGACAGGCGCTTGACGCGCCAGAGGCGCGCTGAGC
 CCAGGAAGAAGAGTGGACACTGAGCCTGAAGAACCTGCGGCGGAGGACAGCGGCAAAATAC
 ACCTGACCGCGTGTGCAAGCGCGCGGGCGCCATCAACGCCACCTACAAGGTGGATGTATCCA
 GGGGACCGCTTCCAAGCCCGTGCTCACAGGCAACGCCCGCTGAACACGACGCTGGACTTCG
 GGGGACCAACGTCCTTCCAGTGCAGGTGGCGAGCGACGTGAAGCCGCTGATCCAGTGGCTG
 AAGCGCGTGGAGTACGCGCGCGAGGGCGCGCAACACTCCACCATCGATGTGGGCGGCCAGAA
 GTTTGTGGTGTCTGCCACCGGAGGAGTACGTGTGTCGCGGCCCGACGGCTCCTAGCTCAATAAGC
 TGCTCATCATCGTGCCTGCGCGCGAGACGATGCGGGCATGTACATGTGCTTGGCGCAACACC
 ATGGGCTACAGCTTCCGCAAGCGCTTCTTCCACCGTGTGCCAGACCCAAAACCGCGAGGCC
 ACCTGTGCTCTCTCTCTCTCTGCGGCACTAGCTGCGTGGCCGTGGTCTCGGATCGGATCCAG
 CCGGCGCTGTCTTATCTCTGGGACCCCTGCTCCTGTGGCTTTGCCAGGCCAGAGAAGCCG
 TGCACCCCGCGCGCTGCCCTCCTCTGCTGGGACCGCCCGCGGGGACGGCCGCGACCG
 CAGCGGAGACAAGGACTTCTCCTCGTGGCGGCCCTCAGCGCTGGCCCTGGTGTGGGGGCTGT
 GTGAGGACATGGGTCTCGGCGAGCCCCCGAGCACTTACTGGGCGCGAGCCAGTTGCTGGC
 CCTAAGTTTACCCCAAACTTACACAGACATCCACACACACACACACACACTTCCACAC
 ACATTCACACGTTGGAGGCAAGGTCCACGACACATCCACTATCAGTGTAGACGCGACCGT
 ATCTGCAGTGGGACCGGGGGGGCGCGCGAGCAGGAGCTGGGAGGATGGAGGAGCGGAGCT
 CGAGACGAAGGCAAGGCAACCATGGCGAGGAGGAATGGCCAGCACCCCGAGGAGCTGTGTG
 TGAGGCATAGCCCTGGACACACACACAGACACACACTACTGGATGATGTATGCAC
 ACACATGGCGCACACGCTGCTCCTGAAGGCACACGTACGCACACGACATGCACAGATATG
 CCGCTGGGACACAGATAAGCTGCCAAATGCACGCACACGCGACAGAGACATGCCAGAAC
 TACAAGGACATGCTGCCGTAACATACACAGCACACCCATGGCGAGATGTGCTGCCGACAC
 CACACACACACACGGATATGCTGTCTGGACGACACACGTCAGATATGGTATCCGGACACA
 CACGTCGACAGATATGCTGCCGACACACAGATAATGCTGCTTGACACACATGCACCGG
 ATATTGCCCTGGACACACACACACACGCGTGCACAGATATGCTGTCTGGACACGACAC
 ACATACAGATATGCTGCTGGACACACACTCCAGACACACGTCACAGGCGAGATATGCT
 GCCTGGACACACGAGATATGCTGTCTAGTCACACACACACGACAGACATGCTGTCCGACAC
 ACACACGATGCACAGATATGCTGTCCGACACACACACGACAGACAGATATGCTGCTGGAC
 CACACACAGATATGCTGTGCCCTCAACACTCACACACGTCAGATATGCTTGGACACACACA
 TGTGCACAGATATGCTGTGGACATGCACACACGTCAGATATGCTGTCCGATACACACG
 CACGACACATGAGATATGCTGCTGGGACACACTTCCGGACACACATGCACACAGGT
 GCAGATATGCTGCTGGACACACACAGATAATGCTGCCCTCACACTCACACAGTGCAGATA
 TATTGCCCTGGACACACACATGTCACAGATATGCTGTCTGGACATGCACACGTCAGATA
 TGCTGTCCGATACACACGCGACACATGCAGATATGCTGCCCTGGGACACACTTCCGATA
 CACACATGCACACACAGGTGCAGATATGCTGCTGGACACGACGAGATGAGTGTGCTTTGG
 GAGGTGTGCCGTGAGCCTGACGTACGTGCGGTGAGGCTCATAGTTGATGGAGGACTTT
 CCTCTGCTCCACCGTCACTCCCCAACTCTGCCCGGCTCTGTCCCCGCTGCTGCTCCCCGCTC
 CATCCCGGCTGTGCTCCTGGCTTGGCGGCTATTTTGGCCACTGCTTGGGTGGCCAGG
 AGTCCCTTACTGTGTGGGTGGGGTGGGGGACAGGACCCCAAGCCTGAGAGGCTGGAG
 CCGATGGCTAGTGGCTCATCCCCAGTGCAATTCCTCCCTGACACAGAGAAGGGGCTTGTA
 TTTATATTTAAGAAATGAAGATAATTAATAATGATGGAAGGAAGACTGGGTGTGAGGAGC
 TGTGGTCTCTCTGGGCGCGGGACCGCGCTGCTTTAGCCATGCTGATGACCAACCC
 GTCCAGGCGACACACACCCCGCCACCCACTGTGCTGGTGGGCGGAGATCTCTGTAAATTTTA
 TGTAGAGTTTGAAGCTGAAGCCCGTATATTTAATTTATTTTGTAAACAGAAAA

FIGURE 70

MTSPSLLLLLLPLLLLGAFPPAAAAAGPPKMADKVVPRQVARLGRTVRLQCFVEGDPPPLTM
WTKDGRTIHSGWSRFRVLPQGLKVKQVEREDAGVYVCKATNGFGLSVNYTLVVLLDDISPGK
ESLGPDSSSGQEDPASQQWARPRFTQPSKMRRRV IARPVGSSVRLKCVASGHPRPDITWMK
DDQALTRPEAAEPRKKKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQRTSRKPV
TGTHPVNTTVDFFGTTTSFQCKVRSDVKPVIQWLKRVEYGAEGRHNSTIDVGGQKFVVLPTGD
VWSRPDGSYLNKLLITRARQDDAGMYICLGANTMGYSFRSAFLTVPDPKPPGPPVASSSSA
TSLPWPVVIGIPAGAVFILGTLLLWLCQAQKKPCTPAPAPPLPGHRPPGTARDRSGDKDLP
LAALSAGPGVGLCEEHGSAPAQHLLGPGPVAGPKLYPKLYTDIHTHTHTSHTHSHVEGKV
HQHIHYQC

[illegible]

FIGURE 72

MVGTKAWVFSFLVLEVTSVLGRQTMLTQSVRRVQPGKKNPSIFAKPADTLESPGEWTTWFNI
 DYPGGKGDYERLDAIRFYGDRVCARPLRLEARTTDWTPAGSTGQVVHGSPEGFWCLNREQ
 RPGQNCSTYTVRFLCPPGSLRRDTERIWSPPSPWSKCSAACGQTGVQTRTRICLAEMVSLCS
 EASEEGQHCHMGQDCTACDLTCPMGQVNADCDACMCQDFMLHGAVSLPGGAPASGAAYLLTK
 TPKLLTQTDSQGRFRIPGLCPDGKSILKITKVKFAPIVLTMPKTSLKAATIKAEFVRAETPY
 MVMNPETKARRAGQSVSLCCKATGKPRPDKYFWYHNDTLLDPSLYKHESKLVLRKLQHQAG
 EYFCKAQSDAGAVKSKVAQLIVTASDETPCNFVPESYLIRLPHDCFQATNSFYVDVGRCPV
 KTCAGQQDNGIRCRDAVQNCGISKTEEREIQCSGYTLPTKVAKESCQRCTETRSIVRGRV
 SAADNGEPMRFGHVYMGNSRVSMGTGYKGTFTLHVPQDTERLVLTFFVDRQLQFVNTTKVLPFN
 KKGSAVFHEIKMLRRKEPITLEAMETNIIPLGEVGEDPMAELEIPSRSFYRQNGEPYIGKV
 KASVTFLDPNISTATAAQTDLNFINDGDTFPLRTYGMFSVDFRDEVTSEPLNAGKVKVHL
 DSTQVKMPEHISTVKLWSLNPDTGLWEEEGDFKFENQRRNKREDRTFLVGNLEIRERRLFNL
 DVPESRRCFVKVRAIRSERFLPSEIQGVVISVINLEPRTGFLSNPRAWGRFDSVITGPNGA
 CVPAFCDQSPDAYSAYVLASLAGEELQAVESSPKFNPNAIGVPQPYLNKLNRYRRTDHEDPR
 VKKTAFAQISMAKPRPNSAEESNGPIYAFENLRACEEAPPSAAHFRFYQIEGDRYDINTVPFN
 EDDPMSWTEEDYLAWWPKPMEFRACYIKVKIVGPLEVNVRSRNMGGTHRRTVGKLYGIRDVRS
 TRDRDQPNVSAACLEFKCSGMLYDQDRVDRTLKVVIPOGSCRRASVNPMLHEYLVNHLPLAV
 NNDTSEYTMLAPLDPLGHNYGIYTVTDQDPRTAKEIALGRCFDGTSDGSSRIMKSNVGVALT
 FNCVERQVGRQSAFYQLQSTPAQSPAAGTVQGRVPSRRQQRASRGQQRGGVVASLRFPRVA
 QQPLIN

FIGURE 73

CTGCAAGTTGTTAAACGCCTAACACACAAGTATGTTAGGCTTCCACCAAAGTCCTCAATATACCTGAATACGCAC
 AATATCTTAACTCTTCATATTGGTTTTGGGATCTGCTTTGAGGTCCCATCTTCATTTAAAAAAAATACAGAG
 ACCCTACCTACCCGTACGCATACATACATATGTTATATATGTAACCTAGACAAAGATCCGAGATCATAAAGC
 AAGCTCTGCTTTAGTTTCCAAGAAGATTACAAGAATTTAGAGATGTTATTGTCGAAGTCCCTCTGCGATTATG
 CCTTTGGGTTACGGTGTCTTCACTGATGCAGCCCTACCCCTTTGGTTTGGGGACATTATGATTTGTTGTAAGAT
 CAGATTTACACCGGAAGAAGGGAAGTTTGGGATTACATGGCTGCCAGCCGGGAATCCACGGACATGACAAATA
 TCTGAAAGTGAAGCTCGATCTCTCGGATATTACCTGTGGAGACCCTCTGAGACGTTCTGTGCAATTGGCAATC
 CCTACATGTGCAATATAGTGTGATGCGAGTACCCCTGAGCTGGCAGACACCCCTGAGCTGATGTTTGAATTT
 GAAGGAAGACATCCCTCCACATTTTGGCAGTCTGCCCTTGGAAAGGATATCCCAAGCCCTCTCCAGTTAAACAT
 CACTCTGTCTTGGAGCAAAACCATTGAGCTAACAGACAACATAGTTATTACCTTTGAATCTGGGCTCCAGACC
 AAATGATCCTGGAGAAGTCTCTCGATTATGGACGAACATGGCAGCCCTATCAGTATTATGCCACAGACTGCTTA
 GATGCTTTTACATGGATCCTAAATCCGTGAAGGATTATCACAGCATACGGTCTTAGAAATCATTGGCAGACA
 AGAGTACTCAACAGGGTATACAAACAAATAGCAAAATTAATCCACTTTGAAATCAAGACAGGTTCCGCGCTTTTGG
 CTGGACCTCGCCTACGCAATATGGCTTCCCTCTACGGACAGCTGGATACAACCAAGAACTCAGAGATTTCTTT
 ACAGTCAAGACCTGAGGATAAGGCTGTTAAAGACCAGCCGTTGGGGAATATTTGTAGATGAGCTACACTTGGC
 ACGCTACTTTTACGCGATCTCAGACATAAAGGTGCGAGGAAGGTGCAAGTGAATCTCCATGCCACTGTATGTG
 TGTATGACAACAGCAATTTGACATGCGAATGTGAGCACAACACTACAGGTCAGACTGTGGGAAATGCAAGAAG
 AATTATCAGGGCCGACCTTTGGAGTCCAGGCTCCTATCTCCCCATCCCAAGGCACTGCAAAATACCTGTATCCC
 CAGTATTTCCAGTATTGGTACGAATGTCTGCGACAACAGCTCCTGCACTGCCAGAACGGAGGACGTCGCCACA
 ACAACGTGCGCTGCTGTGCCCGGCCGCATACAGGGCATCCTCTGCGAGAAGCTGCGGTGCGAGGAGGCTGGC
 AGCTGCGGCTCCGACTCTGGCAGGGCGCGCCCCCGCAGGCAACCCAGCGCTGTGCTGTGACCAAGCTGCT
 GGGAACCGCCAGCCCCCTGGTGTCTAGGTGTCACTCCAGCCACACCGGACGGGCTGTGCGCGTGGGGAAGCA
 GACACAACCCAAACATTTGCTACTAATAGGAAACACACACATACAGACACCCCACTCAGACAGTGTACAAA
 CTAAGAAGGCTAACTGAACTAAGCCATATTTATCACCCGTGGACAGCACATCCGAGTCAAGACTGTTAATTTT
 TGACTCCAGAGGAGTTGGCAGCTGTTGATATTATCACTGCAAAATCACATTGCCAGCTGCAGAGCATATTGGGA
 TTGGAAGGCTGCGACAGCCCCCAACAGGAAAGACAAAACAAACAAATCAACCGACCTAAAAACATTTGGC
 TACTCTAGCGTGGTGGCCCTAGTACGACTCCGCCAGTGTGTGGACCAACAAATAGCATTCCTTGTGCTGAG
 GTGCAATTGTGGCATAAAGAAATCTGTTACAAGCTGCCATATTGGCCTGCTTCCGTCCTGAATCCCTTCCAAC
 CTGTGCTTTAGTGACGTTGCTCTGTAACCTCGTTGGTTGAAAGATTTCTTTGTCTGATGTTAGTGATGCACA
 TGTGTAACAGCCCCCTCAAAGCGCAAGCCAGTCTATACCCCTGTATATCTTAGCAGCACTGAGTCCAGTGCGA
 GCACACACCCCACTACAAGAGTGGCTATAGGAAAAAGAAAGTGTATCTATCTCTTTGTATTCAAATGAAGTT
 ATTTTCTTGAACACTGTAATATGTAGATTTTGTATTATTGCAATTTGCTTACAGACAACTCTGTTAAT
 GTATCTAATTCGAATCAGCAAAAGCTGACATTTTATTTTGTCTCTTCTGTTTGTGTTTCACTGTGCGA
 GATTTCTCTGTAAGGCAACGAAGCTGCTGGCATCAAAGAATATCAGTTTACATATATAACAGTGTATTAAGA
 TCCACCAAGGACATCTAAATGTTTTCTGTGCTTTAACACTGGAAGATTTAAAGATTAATAAATCTCTGCA
 TAAACGATTCAGGAATTTGTATTGCAATTTCTAAGATGAAGGAACAGCCACCAAGCAGTTTCACTCACT
 TTACTGATTTCTGTGTGAGCTGAGTACATTCACTGACGAATTTAGTTCACAGGAGATGGATTGATGTTCACT
 AGCTTGGACAACCTCTGCAAAATATGAGACTATTTCCACTTGGGAAAAATTACAACGCAAAAAA
 AAAAAA

FIGURE 74

MYLSRSLSIHALWVTVSSVMQPYPLVWGHYDLCKTQIYTEEGKVWDYMACQPESTDMTKYLK
 VKLDPPDITCGDPPETFCAMGNPYMCNNECDASTPELAHPPELMFDFEGRHPSTFWQSATWK
 EYPKPLQVNITLSWSKTIELTDNIVITFESGRPDQMILEKSLDYGRTWQPYQYYATDCLDAF
 HMDPKSVKDLSQHTVLEIICTEEYSTGYTTNSKIHFEIKDRFALFAGPRLRNMASLYGQLD
 TTKKLRFDDFTVTDLRIRLLRPVAGEIFVDELHLARYFYAISDIKVRGRCKCNLHATVCVYDN
 SKLTCECEHNTTGPDCKKCKNYQGRPWSPGSYLPKPGTANTCIPSISSIGTNVCDNELLH
 CQNGGTCHNNVRCLCPAAYTGILCEKLRCEEAGSCGSDSGQGAPPHGTPALLLLTLLGTAS
 PLVF



FIGURE 75

CCCACGCGTCCGGGTGACCTGGGCCGAGCCCTCCCGGTGCGCTAAGATTGCTGAGGAGCGG
 CGGGTAGCTGGCAGGCGCCGACTTCCGAAGGCCGCCGTCCGGGCGAGGTGTCCTCATGACTT
 CTCTTGTGGACATGTCCGTGATCTTTTTCCTGCGTGGTACGGGTAAGGGATGGACTGCC
 CCTCTCAGCCTCTACTGATTTTTTACCACACCCAAGATTTTTTGAATGGAGGAGACGGCTCA
 AGAGTTTAGCCTTGGCGACTGGCCCAGTATCCAGGTCGAGGTTCTGCAGAAGGTTGTGACTTT
 AGTATACATTTTTCTTCTTTCGGGGACGTGGCCTGCATGGCTATCTGCTCCTGCCAGTGTCC
 AGCAGCCATGGCCTTCTGCTTCTTGGAGACCTGTGGTGGGAATTCACAGCTTCTATGACA
 CTACCTGCATTGGCCTAGCCTCCAGGCCATACGCTTTTCTGAGTTTGACAGCATCATTAG
 AAAGTGAAGTGGCATTTTAACTATGTAAGTTCCTCTCAGATGGAGTGCAGCTTGGAAAAAT
 TCAGGAGGAGCTCAAGTTGCAGCCTCCAGCGGTTCTCACTCTGGAGGACACAGATGTGGCAA
 ATGGGGTGATGAATGGTCACACACCGATGCACTTGGAGCCTGCTCCTAATTCCGAATGGAA
 CCAGTGACAGCCCTGGGTATCCTCTCCCTCATTTCTCAACATCATGTGTGCTGCCCTGAATCT
 CATTCGAGGAGTTCACCTTGCAAGAACATTCTTTACAGGATCCAAGGAGCTGGTTCTGCTGGT
 TGGACCAAACTCGTGAAGCCAGCCACCCTGACCCAAATGAGGAGAGCTCTGATTCTCCCAT
 CCGGGAGCAGTGATGTCAAACCTTCTGCTGCTGGGGAAATCTCATCAGCAGGGAGCCTGTGGA
 AAAGGCGATGTGAGTAAATCTGGGAATGGCTGGATTGCGAAACATCTGCCCATGTGTATTG
 ATGGCAGAGCTGTGCCCCACAAGCGCCTTTATTTAGGGTAAATTAACAAATCCATTCTAT
 TCCTCTGACCCATGCTTAGTACATATGACCTTTAACCCCTTACATTTATATGATTCTGGGTT
 GCTTCAGAAGTGTTATTTTCATGAATCATTTCATATGATTTGATCCCCAGGATTCTATTTGT
 TTAATGGGCTTTTCTACTAAAAGCATAAAATACTGAGGCTGATTTAGTCAGGGCAAACCAT
 TTAATTTACATATTCGTTTTCAATACTTGTGTTTCATGTTACACAAGCTTCTTACGGTTTTT
 TTGTAACAATAAATATTTTGTAGTAAATAATGGGTACATTTTAACAACTCAGTAGTACAACC
 TAAACTTGATAAAAGTGTGTAAAAATGTATAGCCATTTATATCCTATGTATAAATTAATG
 AGGTGGCTTCAGAAATGGCAGAATAAATCTAAAGTGTATTAAAAA
 AAAAG

FIGURE 76

MSVIFACVVRVVDGLPLSASTDFYHTQDFLEWRRRLKSLALRLAQYPGRGSAEGCDFSIHF
SSFGDVACMAICSCQCPAAMAFCFLET LWWEFTASYDTTCIGLASRPYAFLEFDSIIQVKW
HFNYVSSSQMECSLEKIQEELKLQPPAVLTLEDTDVANGVMNGHTPMHLEPAPNFRMEPVTA
LGILSLILNIMCAALNLIRGVHLAEHSLQDPRSWFCWLDQTS

TGCTTCCTGGAGACCCGTGTGGTGGGAATTCACAGCTTCNTATGACACTACCTGCATTGGCNT
 AGCCTCCAGGCCATACGCTTTTCTTGAGTTTGACAGCATCATTACAGAAAGTGAAGTGGCATT
 TTAACATATGTAAGTTCCTNTCAGATGGAGTGCAGCTTGGAATAAATTCAGGAGGAGCTCAAG
 TTGCAGCCTCCAGCGGTTCTCANTATGGAGGACACAGATGTGGCAAAATGGGGT

FIGURE 78

CTCAGCGGCGCTTCTCGTAGCGAGCCTAGTGGCGGGTGTTTGCATTGAAACGTGAGCGCGA
 CCCGACCTTAAAGAGTGGGGAGCAAAGGGAGGACAGAGCCCTTTAAACGAGGCGGGTGGTG
 CCTGCCCTTTAAGGGCGGGGCGTCCGGACGACTGTATCTGAGCCCCAGACTGCCCCGAGTT
 TCTGTGCGAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGGTGCTTGGCGGCGGCGGCTT
 CCTCCCCGCTCGTCTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTA
TGGAAGCACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGC
 GAGTGTATTATATCAACACTTCTGTTTGAACACTGTACATCCTCTGCCACATCTTCCGTGAC
 CCGCTTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGA
 TTGCGCTCGAGCTGTGCACCTTTACCTTGGCAATTGCCCTGGGTGCTGTCTGCTCCTGCC
 TTCTCCATCATCAGCAATGAGGTGCTGCTCTCCCTGCGCTCGGAACACTACATCAGTGGCT
 CAACGGCTCCCTCATCCATGGCCTCTGGAACCTTGTTTTCTCTTCCCAACCTGTCCCTCA
 TCTTCTCATGCCCCTTGCATATTTCTTCACTGAGTCTGAGGGCTTTGCTGGCTCCAGAAAG
 GGTGTCTTGGGCGGGTCTATGAGACAGTGGTGATGTTGATGCTCCTCACTCTGCTGGTGCT
 AGGTATGTTGTTGGGTGGCATCAGCCATTGTGGACAAGAACAAGGCCAACAGAGAGTCACTCT
 ATGACTTTTGGGAGTACTATCTCCCTACCTCTACTCATGTCATCTCCTTCTTGGGGTTCTG
 CTGCTCCTGGTGCTACTCCACTGGGTCTCGCCCGCATGTTCTCCGTCACTGGGAAGCTGCT
 AGTCAAGCCCCGGCTGCTGGAAGACCTGGAGGACAGCTGTACTGCTCAGCCTTTGAGGAGG
 CAGCCCTGACCCGAGGATCTGTAATCCTACTTCTGCTGGCTGCTCTTTAGACATGGAGCTG
 CTACACAGACAGGTCTGCTGCTGAGACACAGAGGGTCTGCTGGAGAAGAGGCGGAAGGC
 TTCAGCCTGGCAACGGAACCTGGGCTACCCCTGGCTATGCTGTGCTTGTGCTGTGCTGACGG
 GCCTGTCTGTGCTCATTGTGGCCATCCACATCCTGGAGTGTGCTCATCGATGAGGCTGCCATG
 CCCCAGGCGATGACAGGTACCTCCTTAGGCCAGGTCTCCTTCTCCAAGCTGGGCTCCTTTGG
 TGCGTCTATTAGGTTGTACTCATCTTTTACCTAATGGTGTCCCTCAGTTGTGGGCTTCTATA
 GCTCTCCACTCTTCCGGAGGCTGCGGCCAGATGGCAGCACACTGCCATGACGCAGATAATT
 GGGAACTGTGCTGTCTCCTTGGTCTTAAGCTCAGCACTTCCTGTCTTCTCTCAACCCCTGGG
 GCTCACTCGCTTTGACCTGCTGGGTGACTTTGGACGCTTCAACTGGCTGGGCAATTCTTACA
 TTGTGTTCTCTACACGCAAGCCTTTGCAAGGCTCACCACACTCTGCTGGTGAAGACCTTC
 ACTGCAGCTGTGCGGCGAGAGCTGATCCGGGCTTTGGGCTGGACAGACTGCCGCTGCCGCT
 CTCGGTTTCCCCAGGCATCTAGGAAGACCCAGCACCAG**TGAC**CTCCAGCTGGGGGTGGGA
 AGGAAAAAAGTGGACACTGCCATCTGCTGCCTAGGCCTGGAGGGAAGCCCAAGGCTACTTGG
 ACCTCAGGACCTGGAATCTGAGAGGGTGGGTGGCAGAGGGGAGCAGAGCCATCTGCACATT
 GCATAATCTGAGCCAGAGTTTGGGACCAAGGACCTCCTGCTTTTCCATACTTAACGTGGCCT
 CAGCATGGGGTAGGGCTGGGTGACTGGGTCTAGCCCTGATCCCAAACTCTGTTTACACATCA
 ATCTGCCTCACTGCTGTTCTGGGCCATCCCCATAGCCATGTTTACATGATTGATGTGCAAT
 AGGTGGGGTAGGGGAGGGAAAGGACTGGGCGAGGGCAGGCTCGGGAGATAGATTGTCTCC
 CTTGCTCTGGCCACGCAAGCCTAAGCACTGTGCTATCTCGAGAGGGGCTTTGGACCACTG
 AAAGACCAAGGGGATAGGGAGGAGGAGCTTCAGCCATCAGCAATAAAGTTGATCCAGGGA
 AAAAAA

FIGURE 79

MEAPDYEVLSVREQLFHERIRECIISTLLFATLYILCHIFLTRFKKPAEFTTVDDDEDATVNK
 IALELCTFTLAIALGAVLLLPFSIISNEVLLSLPRNYIIQWLNGLIHGLWNLVFLFPNLSL
 IFLMPFAYFFTESEGFAGSRKGVLRVYETVVMLMLLTLLVLGMVWVASAIVDMKNKANRESL
 YDFWEYYLPYLYSCISFLGVLLLLLVCTPLGLARMFSVTGKLLVKPRILLEDLEEQLYCSAFEE
 AALTRRICNPTSCWLPLDMELLHRQVLALQTQRVLLEKRRKASAWQRNLGYPLAMLCLLVLT
 GLSVLIVAIHILELLIDEAAMPGRMQGTSLGQVSFSKLSFGAVIQVVLI FYLMVSSVVGFY
 SSPLFRSLRPRWHDAMTQIIGNCVCLLVLSALPVFSRTLGLTRFDLLGDFGRFNWLGNFY
 IVFLYNAAFAGLTTICLVKTFTA AVRAELIRAFGLDRLPLPVSGFPQASRKTQHQ

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FIGURE 80

GGCTGCCGAGGGAAGGCCCCCTTGGGTTGGTCTTGGTTGCTTGGCGGCGGCGGNTTCNTCCCC
GCTCGTCCTCCCCGGGCCCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGAAGC
ACCTGACTACGAAGTGCTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGTGTA
TTATATCAACACTTCTGTTTGCAACACTGTACATCCTCTGCCACATCTTCCTGACCCGCTTC
AAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCG



FIGURE 81

GACCGACCTTAAAGAGTGGGAGCAAAGGGAGGACAGAGCCTTTTAAACGAGGCGGTGGTG
CTGCCCTTTAAGGGCGGGCGCTCCGGACGACTGTATCTGAGCCCCAGACTGCCCGAGTTTC
TGTCGCAGGCTGCGAGGAAAGGCCCTAGGCTGGGTCTGGTGCTTGGCGGCGCGGCTTCCT
CCCCGTTGTCNTCCCCGGGCCAGAGGCACCTCGGCTTCAGTCATGCTGAGCAGAGTATGGA
AGCACCTGACTACGAAGTGTATCCGTGCGAGAACAGCTATTCCACGAGAGGATCCGCGAGT
GTATTATATCAACACTTCTGTTTGCAACACTGTACATCNTCTGCCACATCTTCCTGACCCGC
TTCAAGAAGCCTGCTGAGTTCACCACAGTGGATGATGAAGATGCCACCGTCAACAAGATTGC
GCTCGAGCTGTGCACCTTTACCCCTGGCAATTGCCCTGGGTGCTGTCTGCTCCTGCCCTTCT
CCATCATCAGCAATGAGGTGCTGCACTCCC

FIGURE 82

GATGTGCTCCTTGGAGCTGGTGTGCAGTGTCTGACTGTAAGATCAAGTCCAAACCTGTTTT
GGAATTGAGGAACTTCTCTTTTGATCTCAGCCCTGGTGGTCCAGGTCTTCATGCTGCTGT
GGGTGATATTACTGGTCCTGGCTCCTGTCA GTGGACAGTTTGCAAGGACACCCAGGCCATT
ATTTTCCTCCAGCCTCCATGGACCACAGTCTTCCAAGGAGAGAGAGTGACCTCACTTGCAA
GGGATTTTCGCTTCTACTCACACAGAAAACAAAATGGTACCATCGGTACCTTGGGAAAGAAA
TACTAAGAGAAAACCCAGACAATATCCTTGAGGTTT CAGGAATCTGGAGAGTACAGATGCCAG
GCCCAGGGCTCCCCCTCTCAGTAGCCCTGTGCACTTGGATT TTTCTTCAGAGATGGGATTTCC
TCATGCTGCCCAGGCTAATGTTGAACTCCTGGGCTCAAGTGATCTGCTCACCTTAGGCCTCTC
AAAGCGCTGGGATTACAGCTTCGCTGATCCTGCAAGCTCCACTTTCTGTGTTTGAAGGAGAC
TCTGTGGTTCTGAGGTGCCGGGCAAAGCGGAAGTAACACTGAATAATACTATTTACAAGAA
TGATAATGTCTGGCATTCTTAAATAAAAGAACTGACTTCCAAAAAAAAAAAAAAAAAAAAA
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MLLWVILLVLAPVSGQFARTPRPIIFLQPPWTTVFQGERVTLTCKGFRFYSPQKTKWYHRYL
GKEILRETPDNILEVQESGEYRCQAQGSPLSSPVHLDIFSSEMGPFAAQANVELLGSSDLLT

FIGURE 84

CAGAAGAGGGGCTAGCTAGCTGTCTCTGCGGACCAGGGAGACCCCGCGCCCCCGGTGT
 GAGGCGGCTCACAGGGCCGGGTGGGCTGGCGAGCCGACGCGCGCGGAGGAGGCTGTGAG
 GAGTGTGTGGAACAGGACCCGGGACAGAGGAACCATGGGCTCCGCAGAACCTGAGCACCTTTT
 GCCTGTGCTGCTATACCTCATCGGGCGGTGATTGCCGGACGAGATTCTATAAGATCTTG
 GGGGTGCCTCGAAGTGCCTCTATAAAGGATATTAAGGCGCTATAGGAACTAGCCCTGCA
 GCTTCATCCCGACCGGAACCTGATGATCCACAAGCCCAGGAGAAATTCAGGATCTGGGTG
 CTGCTTATGAGTTCTGTGAGATAGTGAGAAACGGAACAGTACGATACTTATGGTGAAGAA
 GGATTAAGATGGTCATCAGAGCTCCCATGGAGACATTTTTTACACTTCTTTGGGGATTT
 TGGTTTCATGTTTGGAGGAACCCCTCGTCAGCAAGACAGAAATATCCAAGAGGAAGTGATA
 TTATTGTAGATCTAGAAGTCACCTTGAAGAAGTATATGCAGGAAATTTTGTGGAAGTAGTT
 AGAAACAAACCTGTGGCAAGGCAGGCTCCTGGCAACGGAAGTGCAATTGTGCGCAAGAGAT
 GCGGACCACCCAGCTGGGCGCTTCCAAATGACCCAGGAGGTGGTCTGCGACGAAT
 GCCCTAATGTCAAACAGTGAATGAAGAACGAACGCTGGAAGTAGAAATAGAGCCTGGGGTG
 AGAGACGGCATGGAGTACCCCTTTATTGGAGAAGGTGAGCCTCACGTGGATGGGGAGCCTGG
 AGATTTACGGTTCCGAATCAAAGTTGTCAAGCACCCAATATTTGAAAGGAGAGGAGATGATT
 TGTACACAAATGTGACAATCTCATTAGTTGAGTCACTGGTTGGCTTTGAGATGGATATTACT
 CACTTGGATGGTCACAAGGTACATATTTCCCGGATAAGATCACCAGGCCAGGAGCGAAGCT
 ATGGAAGAAAGGGGAAGGGCTCCCCAECTTTGACAACAACAATATCAAGGGCTCTTTGATAA
 TCACTTTTGATGTGGATTTTCCAAAAGAACAGTTAACAGAGGAAGCGAGAGAAGGTATCAAA
 CAGCTACTGAAACAAGGGTCAGTGCAGAAGGTATACAATGGACTGCAAGGATATTGAGAGTG
 AATAAAATTTGACTTTGTTTTAAATAAGTGAATAAGCGATATTTATTATCTGCAAGGTTTTT
 TTGTGTGTGTTTTTTGTTTTATTTTCAATATGCAAGTTAGGCTTAATTTTTTTATCTAATGA
 TCATCATGAAATGAATAAGAGGGCTTAAGAATTTGTCCATTTGCATTGCGAAAAGAATGACC
 AGCAAAAGGTTTACTAATACCTCTCCCTTTGGGGATTTAATGTCTGGTGTGCCGCTGAGT
 TTCAAGAATTAAGCTGCAAGAGGACTCCAGGAGCAAAAGAAACACAATATAGAGGGTTGGA
 GTTGTGTAGCAATTTCAATTCAAATGCCAAGTGGAGAAGTCTGTTTTTAAATACATTTTGTG
 TTATTTT

FIGURE 85

MAPQNLSTFCLLLLYLIGAVIAGRDFYKILGVPRASIKDIKKAYRKALQLHPDRNPDDPQ
AQEKFDLGAAYEVLSDSEKRRQYDTYGEEGLKDGHQSSHGDI FSHFFGDFGFMFGGTPRQQ
DRNIPRGSDIIVDLEVTLEEVYAGNFVEVVRNKPVARQAPGKRKCNCRQEMRTTQLGPGRFQ
MTQEVVCDCECPNVKLVNEERTLEVEIEPGVRDGMIEYPFIGEGERPHVDGEPGDLRFRIKVVKH
PIFERRGDDLYTNVTISLVESLVGFEMDITHLDGHKVHISRDKITRPGAKLWKKGEGLPNFD
NNNIKGSIIITFDVDFPKEQLTEEAREGIKQLLKQGSVQKVYNGLQGY

Important features:**Signal peptide:**

amino acids 1-22

Cell attachment sequence.

amino acids 254-257

Nt-dnaJ domain signature.

amino acids 67-87

Homologous region to Nt-dnaJ domain proteins.

amino acids 26-58

N-glycosylation site.

amino acids 5-9, 261-265

Tyrosine kinase phosphorylation site.

amino acids 253-260

N-myristoylation site.

amino acids 18-24, 31-37, 93-99, 215-221

Amidation site.

amino acids 164-168

TGGGACCAGGGAACCCCGGGCCCCCGGTGGAGNGCCTAACAGGCCGGTGTGNTGCGACCGAA
GCGGCGGGCGGAGGAGGTTTTGAGGATTTTTGGAACAGGACCCGACAGAGGAACCATGTT
CCGCAGAACNTGAGCAGNTTTTGCTGTGTTGNTGNTATACTTCATCGGGCGGTGATTGCCGG
ACGAGATTTNTATAAGATTTTGGGGTGCCTNAGAGTGCCTTNTATAAAGGATATTTAAAGAG
CCTATAGGAACTAGCCCTGCAGNTTATCCCGACCGGAACCCGTGATGATCCACAAGCCCAG
GAGAAATTCAGGATTTGGGTGCTGCTTATGAGGTTNTGTGAGATAGTGAGAAACGGAACA
GTACGATAATTATGTTGAAGAAGGATTAAGATGGTNATCAGAGCTCCCATGGAGACATTT
TTTACACATNTTTGGGGATTTTGGTTTCATGTTTGGAGGAACCCCTNGTCAGCAAGACAGA
AATATTCCAAGAG

FIGURE 87

GGACACGAGGCGGCGGGGCAGTTCGCGGGATGCGCCCGGAGCCACAGCCTGAGGCCCTCAGGT
 CTCGACAGGTGCTCGTGAGGAACCTAGCACCTGCCATCCTCTTCCCAATTGCCACTTCCA
 GCAGCTTTAGCCCATGAGGAGGATGTGACCGGACTGAGTCAGGAGCCCTCTGGAAGC**ATGG**
 AGACTGTGGTGATTGTTGCCATAGGTGTGCTGGCCACCATCTTTCTGGCTTCGTTTGACGCC
 TTGGTGCTGGTTTGACGGCAGCGCTACTGCCGGCCGCGAGACCTGCTGCAGCGCTATGATTC
 TAAGCCCATTTGGACCTCATTGGTGCCATGGAGACCCAGTCTGAGCCCTCTGAGTTAGAAC
 TGGACGATGTCGTTATCACCAACCCCCACATTGAGGCCATTCTGGAGAATGAAGACTGGATC
 GAAGATGCCTCGGGTCTCATGTCCCACTGCATTGCCATCTTGAAGATTGTACACTCTGAC
 AGAGAAGCTTGTGCCATGACAATGGGCTCTGGGGCCAAGATGAAGACTTCAGCCAGTGTCA
 GCGACATCATTGTGGTGGCCAAGCGGATCAGCCCCAGGGTGGATGATGTTGTGAAGTCGATG
 TACCTCCGTTGGACCCCAAACCTCTGGACGCACGGACGACTGCCCTGCTCCTGTCTGTGACG
 TCACCTGGTGCTGGTGACAAGGAATGCCTGCCATCTGACGGGAGGCCCTGGACTGGATTGACC
 AGTCTCTGTGCGCTGCTGAGGAGCATTTGGAAGTCCTTCGAGAAGCAGCCCTAGCTTCTGAG
 CCAGATAAAAGGCCTCCAGGCCCTGAAGGCTTCCTGCAGGAGCAGTCTGCAATT**TAG**TGCCT
 ACAGGCCAGCAGCTAGCCATGAAGGCCCTGCCGCCATCCCTGGATGGCTCAGCTTAGCCTT
 CTACTTTTTCTATAGAGTTAGTTGTTCTCCACGGCTGGAGAGTTCAGCTGTGTGTCATAG
 TAAAGCAGGAGATCCCCGTCAGTTATGCCTCTTTTGACGTTGCAAACTGTGGCTGGTGAGT
 GGCAGTCTAATACTACAGTTAGGGGAGATGCCATTCACTCTCTGCAAGAGGAGTATTGAAAA
 CTGGTGGACTGTCAGCTTTATTTAGCTCACCTAGTGTTCGCAAGAAAATTGAGCCACCGTCT
 AAGAAATCAAGAGGTTTACATTAAAATTAGAATTTCTGGCCTCTCTCGATCGGTCAGAATG
 TGTGGCAATTCTGATCTGCATTTTCAGAAGAGGACAATCAATTGAAACTAAGTAGGGGTTTC
 TTCTTTTGGCAAGACTTGTACTCTCTCACCTGGCCTGTTTCATTTATTTGTATTATCTGCCT
 GGTCCCTGAGGCGTCTGGGTCTCTCCTCTCCCTTGACAGTTTGGGTTTGAAGCTGAGGAACT
 ACAAAGTTGATGATTTCTTTTTTATCTTTATGCCTGCAATTTTACCTAGCTACCACTAGGTG
 GATAGTAAATTTATACTTATGTTTCCCTCAAAAAAAAAAAAAA

FIGURE 88

METVVIVAIGVLATIFLASFAALVLVCRQRYCRPRDLLQRYDSKPIVDLIGAMETQSEPSEL
ELDDVVITNPHIEAILENEDWIEDASGLMSHCIAILKICHTLTEKLVAMTMGSGAKMKTSAS
VSDIIVVAKRISPRVDDVVKSMYPPLDPKLLDARTTALLSVSHLVLVTRNACHLTGGLDWI
DQSLSAEEHLEVLREAALASEPDKGLPGPEGFLQEQSAI

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FIGURE 89

GCTTCATTTCTCCCGACTCAGCTTCCACCCCTGGGCTTTCCGAGGTGCTTTTCGCCGCTGTCC
CCACCACTGCAGCC**CATG**ATCTCCTTAACGGACACGCAGAAAAATTGGAATGGGATTAACAGGA
TTTGGAGTGTTTTTCCCTGTTCTTTGGAATGATTCTCTTTTTTGACAAAGCACTACTGGCTAT
TGGAAATGTTTTATTTGTAGCCGGCTTGGCTTTTGTAATTGGTTTAGAAAAGAACATTAGAT
TCTTCTTCCAAAAACATAAAATGAAAGCTACAGGTTTTTTTTCTGGGTGGTGTATTTGTAGTC
CTTATTGGTTGGCCTTTGATAGGCATGATCTTCGAAATTTATGGATTTTTTCTCTTGTTCAG
GGGCTTCTTTCCTGTCGTTGTTGGCTTTATTAGAAGAGTGCCAGTCCTTGGATCCCTCCTAAAT
TTACCTGGAATTAGATCATTTGTAGATAAAGTTGGAGAAAGCAACAATATGGTAT**TAA**CAACA
AGTGAATTTGAAGACTCATTTAAATATTTGTGTTATTTATAAAGTCATTTGAAGAATATTCA
GCACAAAATTAATACATGAAATAGCTTGTAAATGTTCTTTACAGGAGTTTAAACGTATAG
CCTACAAAGTACCAGCAGCAAATTAGCAAAGAAGCAGTGAAAACAGGCTTCTACTCAAGTGA
ACTAAGAAGAAGTCAGCAAGCAAAGTGAAGAGGTTGAAATCCATGTTAATGATGCTTAAAGAA
ACTCTTGAAGGCTATTTGTGTTGTTTTCCACAATGTGCGAAACTCAGCCATCCTTAGAGAA
CTGTGGTGCCCTGTTTCTTTTTCTTTTTTGAAGGCTCAGGAGCATCCATAGGCATTTGCT
TTTTAGAAGTGCCACTGCAATGGCAAAAATTTCCAGTTGCACTGTATCTCTGGAAGTGA
TGCATGAATTCGATTGGATTGTGTCATTTAAAGTATTTAAACCAAGGAAACCCCAATTTTG
ATGTATGGATTACTTTTTTTTGNGCNCAGGGCC

FIGURE 90

MISLTDTKIGMGLTGFGVFLLFFGMILFFDKALLAIGNVLEFVAGLAFVIGLERTFRFFFQK
HKMKATGFFLGGVFVVLIGWPLIGMIFEIYGFFLLFRGFFPVVVGFIIRVPVLGSLNLNLPGI
RSFVDKVGESNNMV

Important features:**Transmembrane domains:**

amino acids 12-30 (typeII), 33-52, 69-89 and 93-109

N-myristoylation sites.

amino acids 11-16, 51-56 and 116-121

Aminoacyl-transfer RNA synthetases class-II protein.

amino acids 49-59

FIGURE 91

GAAGACGTGGCGGCTCTCGCCTGGGCTGTTCCCGGCTTCATTTCTCCCGACTCAGCTTCCC
ACCNTGGGCTTTCGAGGTGCTTTCGCCGCTGTCCCCACCACTGCAGCCATGATCTCCTTAA
CGGACACGCAGAAAATTGGAATGGGATTAACCGGATTTGGAGTGTTTTCTGTCTTTGGA
ATGATTCTCTTTTTTGACAAAGCACTACTGGCTATTGGAAATGTTTTATTTGTAGCCGGCTT
GGCTTTTGTAATTGGTTTAGAAAGAACATTCAGATTCTTCTTCCAAAAACATAAAATGAAAG
CTACAGGTTTTTTCTGGGTGGTGTATTTGTAGTCCTTATTGGTTGGCCTTTGATAGGCATG
ATCTTCGAAATTTATGGATTTTTTCTCTTGTTT

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FIGURE 92

GGACAGAGGCTGAACCCAGCCGGCTCCATCTCAGCTTCTGGTTTCTAAGTCCATGTGCCAAA
 GGCTGCCAGGAAGGAGACGCCCTTCTGAGTCTCGATCTTTCTTCTCTGGAATCTTTGA
 CTGTGGGTAGTTATTTATTTCTGAATAAGAGCGTCCACGCATCCATGACCTCGCGGGACTGC
 TGAAGTCTCAGTTCCTGTGCCACCTGGTCTTCTGCTACGTCTTTATTGCCTCAGGGCTAATC
 ATCAACACCATTACAGTCTTCACTCTCCTCCTCTGGCCCATTAACAAGCAGCTCTTCGGAA
 GATCAACTGCAGACTGTCTATTGCATCTCAAGCCAGCTGGTGATGCTGCTGGAGTGGTGGT
 CGGGCACGGAATGCACCATCTTACGGACCCGCGCCTACCTCAAGTATGGGAAGGAAAAAT
 GCCATCGTGGTTCTCAACCACAAGTTTGAAATTGACTTTCTGTGTGGCTGGAGCCTGTCCGA
 ACGCTTTGGGCTGTTAGGGGGCTCCAAGGTCTTGCCAAAGAAAGAGCTGGCCTATGTCCCAA
 TTATCGGCTGGATGTGGTACTTCACCGAGATGGTCTTCTGTTTCGCGCAAGTGGGAGCAGGAT
 CGCAAGACGGTTGCCACCAGTTTGCAGACCTCCGGGACTACCCCGAGAAGTATTTTTCTCT
 GATTCAGTGTGAGGGACACGGTTACAGGAGAAGAAGCATGAGATCAGCATGCAGGTGGCCC
 GGGCCAAGGGGCTGCCTCGCCTCAAGCATCACCTGTTGCCACGAACCAAGGGCTTCGCCATC
 ACCGTGAGGAGCTTGAGAAATGTAGTTTCAGCTGTATATGACTGTACACTCAATTTAGAAA
 TAATGAAAATCCAACACTGCTGGGAGTCCCTAAACGGAAAGAAATACCATGCAGATTGTATG
 TTAGGAGGATCCCACTGGAAGACATCCCTGAAGACGATGACGAGTGTCTGGCCTGGCTGCAC
 AAGCTCTACCAGGAGAAGGATGCCTTTACAGGAGGAGTACTACAGGACGGGCACCTTCCAGAG
 GACGCCCATGGTGCCCCCGGCGGCCCTGGACCTCGTGAACCTGGCTGTTTTGGGCCCTCGC
 TGGTGCTCTACCTTTCTTCCAGTTCTCTGGTCAGCATGATCAGGAGCGGGTCTTCCCTGACG
 CTGGCCAGCTTCATCCTCGTCTTCTTTGTGGCCTCCGTGGGAGTTCGATGGATGATTGGTGT
 GACGGAATTTGACAAGGGCTCTGCCTACGGCAACTCTGACAGCAAGCAGAACTGAATGACT
GACTCAGGAGGTGTACCATCCGAAGGGAACCTTGGGGAAGTGGTGGCCTCTGCATATCCT
 CCTTAGTGGGACACGGTGACAAAGGCTGGGTGAGCCCCGTCTGGGCACGGCGGAAGTCACGA
 CCTCTCCAGCCAGGGAGTCTGGTCTCAAGGCCGATGGGGAGGAAGATGTTTTGTAATCTTT
 TTTTCCCATGTGCTTTAGTGGGCTTTGGTTTTCTTTTGTGCGAGTGTGTGTGAGAATGGC
 TGTGTGGTGAGTGTGAACCTTTGTCTGTGATCATAGAAAGGGTATTTTAGGCTGCAGGGGAG
 GGCAGGGCTGGGGACCGAAGGGGACAAGTTCCCTTTTCATCCTTTGGTGTGAGTTTTCTGT
 AACCTTGGTTGCCAGAGATAAAGTGAAAAGTGCTTTAGGTGAGATGACTAAATATGCCTC
 CAAGAAAAAAAATTAAGTGCTTTTCTGGGTCAAAAAA

FIGURE 94

CTGAGCGGGCGGTAGC**ATG**GAGGGGAGAGTACGTCGGCGGTGCTCTCGGGCTTTGTGCTCG
 GCGCACTCGCTTTCCAGCACCTCAACACGGACTCGGACACGGAAGGTTTTCTTCTGGGGAA
 GTAAAAGGTGAAGCCAAGAACAGCATTACTGATTCCTCCAAATGGATGATGTTGAAGTTGTTTA
 TACAATTGACATTCAGAAATATATTCATGCTATCAGCTTTTCTAGCTTTTATAATTCTTCAG
 GCGAAGTAAATGAGCAAGCACTGAAGAAAATATTATCAAATGTCAAAAAGAATGTGGTAGGT
 TGGTACAAATTCGTCGTCATTGATCAGATCATGACGTTTATAGAGAGAGGCTGCTTCACAA
 AAAGTTCAGGAGCATTTTTCAAACCAAGACCTTGTTTTTCTGCTATTAACACCAAGTATAA
 TAACAGAAAGCTGCTCTACTCATCGACTGGAACATTCTTATATAAACCTCAAAAAGGACTT
 TTTCACAGGTACCTTTAGTGGTTGCCAATCTGGGCATGTCTGAACAACTGGGTATAAAAC
 TGTATCAGGTTCTGTATGTCCACTGGTTTTAGCCGAGCAGTACAAACACACAGCTCTAAAT
 TTTTTGAAGAAGATGGATCCTTAAAGGAGGTACATAAGATAAATGAATGTATGCTTCATTA
 CAAGAGGAATTAAGAGTATATGCAAAAAAGTGAAGACAGTGAACAAGCAGTAGATAAACT
 AGTAAAGGATGTAACAGATTAACGAGAAATTGAGAAAAGGAGAGGAGCACAGATTGAGG
 CAGCAAGAGAGAAGAACATCAAAAAAGACCTCAGGAGAACATTTTTCTTTGTGAGGCATTA
 CGGACCTTTTTCCAAATCTGAATTTCTTCATTCATGTGTTATGTCTTTAAAAATAGACA
 TGTTCCTAAAAGTAGCTGTAACATAACCAACATCTCGATGTAGTAGACAATCTGACCTTAA
 TGGTAGAACACACTGACATTCCTGAAGCTAGTCCAGCTAGTACACCACAAATCATTAAGCAT
 AAAGCCTTAGACTTAGATGACAGATGGCAATTCAAGAGATCTCGGTTGTTAGATACACAAGA
 CAAACGATCTAAAGCAAATACTGGTAGTAGTAACCAAGATAAAGCATCAAAATGAGCAGCC
 CAGAAACAGATGAAGAAATGAAAAGATGAAGGGTTTTGGTGAATATTCACGGTCTCTTACA
 TTT**TGA**TCCTTTTAACTTACAAGGAGATTTTTTATTGGCTGATGGGTAAAGCCAAACAT
 TTCTATTGTTTTTACTATGTTGAGCTACTTGCAGTAAGTTCATTTGTTTTTACTATGTTTAC
 CTGTTTGCAGTAATACACAGATAACTCTTAGTGCATTTACTTCACAAAGTACTTTTTCAAAC
 ATCAGATGCTTTTATTTCAAACCTTTTTTTTACCTTTTCACTAAGTTGTTGAGGGGAAGGCT
 TACACAGACACATTCTTTAGAATTGGAAGTGAAGACAGGACAGTGGCTCACACCTGTAA
 TCCAGCACTTAGGGAAGACAAGTCAGGAGGATTGATTGAAGCTAGGAGTTAGAGACCAGCC
 TGGGCAACGTATTGAGACCATGCTATTAAAAAATAAAATGGAAGCAAGAATAGCCTTAT
 TTTCAAAATATGGAAGAAATTTATATGAAATTTATCTGAGTCATTAAAAATTCCTCTTAAG
 TGATACTTTTTTAGAAGTACATTATGGCTAGAGTTGCCAGATAAAATGCTGGATATCATGCA
 ATAAATTTGCAAAACATCATCTAAATTTAAAAAAAAAAAAAAAAAAAAA

MEGESTSAVLGGFVLGALAFQHLNTDSDTEGFLLEGVKGAEKNSITDSQMDDEVVYTIIDIQ
KYIPCYQLFSFYNSSGEVNEQALKKILSNVKNVVGWYKFRHSDQIMTFRERLLHKNLQEH
FSNQDLVFLLLTSPSIITESCSTHRLHSLYKPKQGLFHRVPLVVANLGMSEQLGKYTVSGSC
MSTGFSRAVQTHSSKFFEEEDGSLKEVHKINEMYASLQEELKSICKKVEDSEQAVDKLVKDVN
RLKREIEKRRGAQIQAAAREKNIQKDPQENIFLCIQALRHTFFPNSEFLHSCVMSLKNRHVSKSS
CNYNHLDVNDNLTMVEHTDIPEASFASTPFIKHKALDLDDRWFQKSRLLDTQDKRKA
NTGSSNQDKASKMSSPTEDEIEKMGFGFEYSRSTPF

FIGURE 96

GGCACAGCCGCGCGCGGAGGGCAGAGT/CAGCCGAGCCGAGTCCAGCCGGACGAGCGGACCAGCGCCAGGGCAGC
 CCAACAGCCGCGCAGCGAAGCCCGCCGCGCCCAACCCCTCTGCGGTCGCCGCGCGCCTGCCACCCCTTCCCT
 CCTTCCCCCGCTCCCGCCTCGCCGGCCAGT/CAGCTTGCCGGGTTGCTGCCCCCGGAAACCCCGAGGTCACCA
 GCGCGCGCTCTGCTTCCCTGGCCGCGCGCCGCTCCAGCCCTCCTTCTCCCTTGGCCGGCGCTGCCACC
 GGGGACCGTTGCTGACGCGAGGGCCGCGCAGCTCTACTTTTCCGCCCGCGCTCTCTCCGCTGCTCGCCTCTTCCAC
 CAACTCCAACTCCTTCTCCCTCCAGCTCCACTCGCTAGTCCCGACTCCGCGCAGCCTCGGCCGCGCTCGCCGTAG
 CGCGCTTCCCTTCCGTTCCAAAGGTGGGAACGCGTCCGCCCGCGCCGACCA**ATG**GACCGGTTCCGGCTTGCC
 CGCGCTTCTCTGCACCTTGGCAGTGCTCAGCGCCGCGCTGCTGGCTGCCGAGCTCAAGTCGAAAGTTGCTCGG
 AAGTGGCAGCTCTTACGTGTCCAAGGCTTCAACAAGACGATGCCCCCTCCACGAGATCAACGGTGATCAT
 TTGAAGATCTGTCCCCAGGGTCTACCTGCTGCTCTCAAGAGATGGAGGAGAAATACAGCCTGCAAAAGTAAAGA
 TGATTTCAAAGTGTGGTCAGCGAACAGTGCAATCATTTGCAAGCTGTCTTTGCTTACAGTTACAAGAGTTTG
 ATGAATTCCTCAAAGAACTACTTGAAAATGCAGAGAAATCCCTGAATGATATGTTTGTGAAGACATATGGCCAT
 TTATACATGCAAAATCTGAGCTATTTAAGATCTCTTCGTAGAGTTGAAACGTTACTACGTGGTGGGAAATGT
 GAACCTGGAGAAATGCTAAATGACTTCTGGGCTCGCCTCCTGGAGCGGATGTCCGCTGGTGAACCTCCAGT
 ACCACTTTACAGATGAGTATCTGGAATGTGTGAGCAAGTATACGGAGCAGCTGAAGCCCTTCGGAGATGTCCT
 CGCAAATGAAGCTCCAGGTTACTCGTGCTTTGTAGCAGCCGCTACTTTCGCTCAAGGCTTAGCGGTTGCGGG
 AGATGCTGCTGAGCAAGGTCTCGTGTTAAACCCACAGCCAGTGATCCCATGCCCTGTTGAAGATGATCTACT
 GCTCCCATGCCGGGCTCTCGTGACTGTGAAGCCATGTTACAACACTACTGCTCAAACATCATGAGAGGCTGTTTG
 GCCAACCAAGGGGATCTCGATTTTGAATGGAACAATTTTCATAGATGCTATGCTGATGGTGGCAGAGAGGCTAGA
 GGGTCCCTTCAACATGAACTCGGTATGGATCCCATCGATGTGAAGATTTCTGATGCTATTATGAACATGCAGG
 ATATAGTGTTCAAGTGCTCAGAAGGTTTCCAGGGATGTGACCCCCCAAGCCCTCCAGCTGGACGAAAT
 TCTCGTTCATCTCTGAAAGTGCTTCACTGCTCGCTTCAAGACACATCACCCCGAGGAACGCCCAACCAAGC
 AGCTGGCCTAGTTTGAACGACTGGTTACTGATGTCAAGGAGAACTGAAACAGGCCAAGAAATCTGCTCT
 CCCTTCGAGCAACGTTTGCAACGATGAGAGGATGGCTGCAAGAAACGGCAATGAGGATGACTGTTGGAATGG
 AAAGGCAAAAGCAGGTACCTGTTGCACTGACAGGAAATGGATTAGCCAAACGAGGCAACACCCAGAGGTCCA
 GGTTGACACCAGCAAAACAGACATACCTGATCCTTCGTCAAATCATGGCTCTTCGAGTGATGACCAAGATGA
 AGAATGCATACATGGGACAGAGTGGACTTCTTGATATCAGTGATGAAAGTGTGGAGAGGAGTGGAAAT
 GGCTGTGAGTATCAGCAGTGGCTTCCAGTCTGAGTACAATGCCACTGACCATGCTGGGAAGAGTGCCAAATGA
 GAAAGCCGACAGTGCTGGTGTCCGCTCGGGGACAGGCCCTACCTCCTCACTGTCTTCGCATCTTGTCTCGTGG
 TTATGACAGAGAGTGGAGAT**TAAT**TTCTCAAACCTCTGAGAAAAGTGTTCATCAAAAAGTAAAGGCCACAGTT
 ATCACTTTTCTACCTCCTAGTGACTTTGCTTTTAAATGAATGGACAAACATGTACAGTTTCTACTATGTGGC
 CACTGGTTTAAAGAGTGGCTGACTTTGTTTCTCATTGAGTTTGGGAGGAAAAGGACTGTCATTTGAGTTGGT
 TCCCTGCTCCCCAAACCATGTAAACGTGGCTAACAGTGTAGGTACAGAACTATAGTTAGTTGTGCATTTGTGA
 TTTTATCACTCATTAATTGTTGTATGTTTCTCATTTCGTTTGGGTTTGGTTTTCCAACTGTGATCT
 CGCCTTGTTCCTACAGCAACACAGGTCCTCTTGGCAGCTAACATGTACCTATTCTTGAAATATTAATA
 GCTGTACAGAGCAGGTTTATTATCATGTTATCTTATTAAGAAAAAGCCCAAAAGC

FIGURE 97

MARFGLPALLCTLAVLSAALLAELKSKSCSEVRRLYVSKGFNKNDAPLHEINGDHLKICPQ
GSTCCSQEMEEKYSLQSKDDFKSVVSEQCNHLQAVFASRYKKFDEFFKELLENAEKSLNDMF
VKTYGHLYMQNSELFKDLFVELKRYVVGNNLEEMLNDFWARLLERMFLVNSQYHFTDEY
LECVSKYTEQLKPPFGDVPRKLKLQVTRAFVAARTFAQGLAVAGDVVSKVSVVNPTAQCTHAL
LKMIYCSHCRGLVTVKPCYNYCSNIMRGCLANQGDLDFEWNNFIDAMLMVAERLEGPFNIES
VMDPIDVKISDAIMNMQDNSVQVSQKVFQCGCPPKPLPAGRISRSISESAFSARFRPHHPPEE
RPTTAAGTSLDRLVTDVKEKLQAKKFWSSLP SNVCNDERMAAGNGNEDDCWNGKGKSRYLE
AVTGNGLANQGNNPEVQVDTSKPDILILRQIMALRVMTSKMKNAYNGNDVDFDISDESSGE
GSGSGCEYQQCPSEFDYNATDHAGKSANEKADSAGVRPGAQAYLLTVFCILFLVMQREWR

FIGURE 98

CTCGCCCTCAAATGGGAACGCTGGCCTGGGACTAAAGCATAGACCACCAGGCTGAGTATCCT
GACCTGAGTCATCCCCAGGGATCAGGAGCCTCCAGCAGGGAACCTTCCATTATATTCTTCAA
GCAACTTACAGCTGCACCGACAGTTGCGATGAAAGTTCTAATCTCTTCCCTCCTCCTGTTGC
TGCCACTAATGCTGATGTCCATGGTCTCTAGCAGCCTGAATCCAGGGTTCGCCAGAGGCCAC
AGGGACCGAGGCCAGGCTTCTAGGAGATGGCTCCAGGAAGGCGGCCAAGAATGTGAGTGCAA
AGATTGGTTCCTGAGAGCCCCGAGAAGAAAATTTCATGACAGTGTCTGGGCTGCCAAAGAAGC
AGTGCCCCCTGTGATCATTTCAAGGGCAATGTGAAGAAAACAAGACACCAAAGGCACCACAGA
AAGCCAAACAAGCATTCCAGAGCCTGCCAGCAATTTCTCAAACAATGTCAGCTAAGAAGCTT
TGCTCTGCCTTTCTAGGAGCTCTGAGCGCCCACTCTTCCAATTAACATTCTCAGCCAAGAA
GACAGTGAGCACACCTACCAGACACTCTTCTTCTCCACCTCACTCTCCACTGTACCCACC
CCTAAATCATTTCCAGTGCTCTCAAAAAGCATGTTTTTCAAGATCATTTTGTGTTGTGCTCTC
TCTAGTGTCTTCTTCTCTCGTCAGTCTTAGCCTGTGCCCTCCCTTACCCAGGCTTAGGCTT
AATTACCTGAAAGATTCCAGGAAACTGTAGCTTCCTAGCTAGTGTATTTAACCTTAAATGC
AATCAGGAAAGTAGCAAACAGAAGTCAATAAATATTTTAAATGTCAAAAAAAAAAAAAAAAAA

FIGURE 99

MKVLISL L L L L L P L M L M S M V S S S L N P G V A R G H R D R G Q A S R R W L Q E G G Q E C E C K D W F L R A P R R
K F M T V S G L P K K Q C P C D H F K G N V K K T R H Q R H H R K P N K H S R A C Q Q F L K Q C Q L R S F A L P L

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FIGURE 100

AATGGCTGTCTTAGTACTTCGCCTGACAGTTGTCCTGGGACTGCTTGTCTTATTCCTGACCT
GCTATGCAGACGACAAACCAGACAAGCCAGACGACAAGCCAGACGACTCGGGCAAAGACCCA
AAGCCAGACTTCCCCAAATTCCTAAGCCTCCTGGGCACAGAGATCATTGAGAATGCAGTCGA
GTTTCATCCTCCGCTCCATGTCCAGGAGCACAGGATTTATGGAATTTGATGATAATGAAGGAA
AACATTTCATCAAAG**TGA**CATCCTCAGGACACACCCATGTGGCTCCTGGACAATCCAAGAGCA
GCCAAATCCTGCTTTTCCAGTTTGGCTCCACAAGTCCTCCAGGACAGAGCCCTCAAAGCAAC
TCCCAACGAGTTCTCAGGATTCAGGCTCTGGCTTCAACCAAAACAGAACTCATTTTGAACACC
CTGACTGCATTTTGTCTTTTAGAAAAGTTAGAATAAAATATGGCGCTTTGGGATCACATAGTTG
ATGGAGAGGAAA



101/330

FIGURE 101

MAVLVLRRLTVVLGLLVLFITCYADDKPKDPDDKPDGKDPDFPKFLSLLGTEIIENAVE
FILRSMRSRSTGFMEFDDNEGKHSSK

101/330

FIGURE 102

GGACGCCAGCGCCTGCAGAGGCTGAGCAGGAAAAAGCCAGTGCCCCAGCGGAAGCACAGCT
 CAGAGCTGGTCTGCC**ATG**GACATCCTGGTCCCACCTCTGCAGTGCTGGTGTCTTCTTAC
 CCTGCCCCCTGCACCTCATGGCTCTGCTGGGCTGCTGGCAGCCCTGTGCAAAAGCTACTTCC
 CCTACCTGATGGCCGTGCTGACTCCCAAGAGCAACCGCAAGATGGAGAGCAAGAAACGGGAG
 CTCCTTCAGCCAGATAAAGGGGCTTACAGGAGCCTCCGGGAAAGTGGCCCTACTGGAGCTGGG
 CTGCGGAACCGGAGCCAACCTTTCAGTTCTACCCACCGGGCTGCAGGGTCACCTGCCTAGACC
 CAAATCCCCACTTTGAGAAGTTCCTGACAAAGAGCATGGCTGAGAACAGGCACCTCCAATAT
 GAGCGGTTTGTGGTGGCTCCTGGAGAGGACATGAGACAGCTGGCTGATGGCTCCATGGATGT
 GGTGGTCTGCACTCTGGTGTCTGTGCTCTGTGCAGAGCCCAAGGAAGGTCCTGCAGGAGGTCC
 GGAGAGTACTGAGACCGGGAGGTGTGCTCTTTTCTGGGAGCATGTGGCAGAACCATATGGA
 AGCTGGGCCTTCATGTGGCAGCAAGTTTTCGAGCCACCTGGAACACATTGGGGATGGCTG
 CTGCCTCACCAGAGAGACCTGGAAGGATCTTGAGAACGCCAGTTCTCCGAAATCCAAATGG
 AACGACAGCCCCCTCCCTTGAAGTGGCTACCTGTTGGGCCCCACATCATGGGAAAGGCTGTC
 AAACAATCTTTCCCAAGCTCCAAGGCACTCATTTGCTCCTTCCCCAGCCTCCAATTAGAACA
 AGCCACCCACAGCCTATCTATCTTCCACTGAGAGGGAC**TAG**CAGAATGAGAGAAGACATT
 CATGTACCACCTACTAGTCCCTCTCTCCCCAACCTCTGCCAGGGCAATCTCTAACTTCAATC
 CCGCCTTCGACAGTGAAAAAGCTCTACTTCTACGCTGACCCAGGGAGGAAACACTAGGACCC
 TGGTTGTATCCTCAACTGCAAGTTTCTGGACTAGTCTCCCAACGTTTGCTCCCAATGTTGTC
 CCTTTCCTTCGTTCCCATGGTAAAGCTCCTCTCGCTTTCCTCCTGAGGCTACACCCATGCGT
 CTCTAGGAACTGGTCACAAAAGTCATGGTGCCTGCATCCCTGCCAAGCCCCCTGACCCCTCT
 CTCCCCACTACCACCTTCTTCTGAGCTGGGGCACCAGGGAGAATCAGAGATGCTGGGGAT
 GCCAGAGCAAGACTCAAAGAGGCAGAGGTTTTGTTCTCAAATATTTTTTAATAAATAGACGA
 AACCACG

MDILVPLLQLLVLLLLILPLHLMALLGCWQPLCKSYFPYLMAVLTPKSNRKMESKKRELFSQI
KGLTGASGKVALELGCCTGANFQFYPPGCRVTCCLDPNPHFEKFLTSMÅENRHLQYERFVV
APGEDMRQLADGSMDDVVVCTLLRLCSVQSPRKVLQEVRRVLRPGGVLFWEHVAEYPGSWAFM
WQQVFEPETHKHIGDGCCLTRVTKDLNQAQFSEIQMERQYFPLKVLPGVPHIMGKAVKQSF
SSKALICSFWSLOLEACTHQPILPLRGT

FIGURE 104

GTGGGATTATTGTAGTGCAAGATCGTTTTCTCAGTGGTGGTGGAAAGTTGCCTCATCGCAGG
 CAGATGTTGGGGCTTTGTCCGAACAGCTCCCTCTGCCAGCTTCTGTAGATAAGGGTTAAAA
 ACTAATATTTATATGACAGAAGAAAAAGATGTCATTCCGTAAAGTAAACATCATCATCTTGG
 TCCTGGCTGTTGCTCTCTTCTTACTGGTTTTGCACCATAACTTCCTCAGCTTGAGCAGTTTG
 TTAAGGAATGAGGTTACAGATTCAGGAATTGTAGGGCC¹TCAACCTATAGACTTTGTCCCAAA
 TGCTCTCCGACATGCAGTAGATGGGAGACAAGAGGAGATTCTCTGTGGTCATCGCTGCATCTG
 AAGACAGGCTTGGGGGGGCCATTGCAGCTATAAACAGCATTACGCACAACACTCGCTCCAAT
 GTGATTTTCTACATTGTTACTCTCAACAATACAGCAGACCATCTCCGGTCTGGCTCAACAG
 TGATTCCCTGAAAAGCATCAGATACAAAATTGTCAATTTTGACCC²TAAACTTTTGAAGGAA
 AAGTAAAGGAGATCTTGACCAGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTAC
 TTGCCAATTCTGGTTC³CCAGCGCAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCA
 AGGTGATATTCTTGCCCTTTACAATACAGCACTGAAGCCAGGCATGCAGCTGCATTTTCAG
 AAGATTGTGATTGAGCTCTACTAAAGTTGTATCCGTGGAGCAGGAAACAGTACAATTAC
 ATTGGCTATCTTGACTATAAAAAGGAAAGAATTCTGAAGCTTTCCATGAAAGCCAGCACTTG
 CTCATTTAATCTGGAGTTTTTGTGCAAACCTGACGGAATGGAAACGACAGAATATACTA
 ACCAACTGGAAAAATGGATGAACTCAATGTAGAAGAGGGA⁴CTGTATAGCAGAACCC⁵TGGCT
 GGTAGCATCACAAACCTCCTCTGCTTATCGTATTTTATCAACAGCACTCTACCATCGATCC
 TATGTGGAATGTCCGCCACCTTGGTTCAGTGCTGGAAAACGATATTCACCTCAGTTTGTA
 AGGCTGCCAAGTTACTCCATTGGAATGGACATTTGAAGCCATGGGGAAGGACTGCTTCATAT
 ACTGATGTTTGGGAAAAATGGTATATTCCAGACCCAAACAGGCCAAATTCAACCTAATCCGAAG
 ATATACCGAGATCTCAAACATAAAGTGA⁶AAACAGAATTGAAC⁷TGAAGCAAGCATTTCTCAG
 GAAGTCCTGGAAGATAGCATGCATGGGAAGTAACAGTTGCTAGGCTTCAATGCCTATCGGTA
 GCAAGCCATGGAAAAAGATGTGTCAGCTAGGTAAAGATGACAACTGCCCTGTCTGGCAGTC
 AGCTTCCAGACAGACTATAGACTATAAATATGTCTCCATCTGCCTTACCAAGTGT⁸TTTCTT
 ACTACAATGCTGAATGACTGGAAAGAAGAACTGATATGGCTAGTTCAGCTAGCTGGTACAGA
 TAATTCAAAC⁹TGCTGTTGGTTTTAATTTTGTAACTGTGGCCTGATCTGTAAATAAACTT
 ACATTTTT¹⁰C

FIGURE 105

MSFRKVNIIILVLAVALFLLVLHHNFLSLSSLLRNEVTDSGIVGPQPIDFVPNALRHAVDGR
QEEIPVVIAASEDRLGGAIAAINSIQHNTRSNIYIIVTLNNTADHLRSWLNSDSLKSIRYK
IVNFDPKLLEGKVKEPDQGESMKPLTFARFYLPILVPSAKKAIYMDDDVIVQGDILALYNT
ALKPGHAAAFSEDCDSASTKVIVIRGAGNQYNYIGYLDYKKERIRKLSMKASTCSFNPGVFVA
NLTEWKRQNITNQLEKWMKLNVEEGLYSRTLGSITTPPLLIVFYQQHSTIDPMWNVRLGS
SAGKRYSPQFVKAALLHWNGHLKPWGRTASYTDVWEKWYIPDPTGKFNLIRRYTEISNIK



FIGURE 106

TGGTTTTTGCCCCATAAATTCCTCAGCTTGAGCAGTTTGTTAAGGAATGAGGTTACAGATT
CAGGAATTNTAGGNCCTCAACCTNTAGANTTTGTCCCAAATGTTCTCCGACATGCAGTAGAT
GGGAGACAAGAGGAGATTCTGTGGTCATCGCTGCATNTGAAGACAGGCTTGGGGGGCCAT
TGCAGCTATAAACAGCATTTCAGCACAACTCGNTCCAATGTGATTTTCTACATTGTTACTC
TCAACAATACAGCAGACCATNTCCGGTCCTGGNTCAACAGTGATTCCTGAAAAGCATCAGA
TACAAAATTGTCAATTTTGACCCATAAATTTTGAAGGAAAAGTAAAGGAGGATCCTGACCA
GGGGGAATCCATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTCCTGGTTCCAGCG
CAAAGAAGGCCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTAC
AATACAGCACTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTCAGCCTCTAC
TAAAGTTGTCATCCGTGGAGCAGGAAA

FIGURE 107

CGACGCTCTAGCGTTTACCGCTGCGGGCTGGCTGGGCGTAGTGGGGCTGCGCGGCTGCCACG
 GAGCTAGAGGGCAAGTGTGCTCGGCCAGCGTGCAGGGAACGCGGGCGGCCAGACAACGGGC
 TGGGCTCCGGGGCCTCGGCGCGGGCGCTGAGCTGGCAGGGCGGGTCGGGCGCGGGCTGCA
 TCCGCATCTCCTCCATCGCCTGCAGTAAGGGCGGGCGCGGCGAGCCTTTGAGGGGAACGACT
 TGTGCGAGCCCTAACAGGGGTGTCTCTGAGCCTGGTGGGATCCCCGAGCGTCACATCACT
 TTCCGATCACTTCAAAGTGGTTAAAACTAATATTATATGACAGAAGAAAAAGATGTCATT
 CCGTAAAGTAAACATCATCATCTTGGTCTGGGCTGTTGCTCTCTTCTACTGGTTTTGCAC
 CATAACTTCTCAGCTTGAGGCAGTTTGTAAAGGAATGAGGTTACAGATTGAGGAATTGTAG
 GGCCTCAACCTATAGGACTTTGTCCCAATGCTCTCCGACATGCAGTAGATGGGAGACAAGA
 GGAGATTCTGTGGTCATCGCTGCATCTGAAGACAGGCTTGGGGGGGCCATTGCAGCTATAA
 ACAGCATTGAGACAACACCTCGCTCCAATGTGATTCTTCTACATGTTACTCTCAACAATACA
 GCAGACCATCTCCGGTCTGGGCTCAACAGTGATTCCCTGAAAAGCATCAGATACAAAATTG
 TCAATTTTGACCCATAACTTTTGAAGGAAAAGTAAAGGAGGATCCTGACCAGGGGGAATCC
 ATGAAACCTTTAACCTTTGCAAGGTTCTACTTGCCAATTTCTGGGTTCCCAGCGCAAAGAAGG
 CCATATACATGGATGATGATGTAATTGTGCAAGGTGATATTCTTGCCCTTTACAATACAGCA
 CTGAAGCCAGGACATGCAGCTGCATTTTCAGAAGATTGTGATTCAGCCTCTACTAAAGTTGT
 CATCCGTGGAGCAGGAACAGTACAATTACATTGGCTATCTTGACTATAAAAAGGAAAGAA
 TTCGTAAGCTTTCCATGAAAGCCAGCACTTGCTCATTTAATCCTGGAGTTTTTGTGCAAAC
 CTGACGGAATGGAACAGCAGAATATAACTAACCAACTGGAAAAATGGATGAAACTCAATGT
 AGAAGAGGGACTGTATAGCAGAACCCTGGCTGGTAGCATCACAACACCTCCTCTGCTTATCG
 TATTTTATCAACAGCACTCTACCATCGATCCTATGTGGAATGTCCGCCACCTTGGTTCAGT
 GCTGGAAAACGATATTACCTCAGTTTGTAAAGGCTGCCAAGTTACTCCATTGGAATGGACA
 TTTGAAGCCATGGGGAAGGACTGCTTCATATACTGATGTTTGGGGAATAATGGTATATTCCA
 GACCCAACAGGCAAAATCAACCTAATCCGAAGATATACCGAGATCTCAAACATAAAGTGAAA
 CAGAAATTTGAACGTGAAGCAAGCATTTCTCAGGAAGTCCCTGGAAGATAGCATGCGTGGGAAG
 TAACAGTTGCTAGGCTTCAATGCCTATCGGTAGCAAGCCATGGAAAAAGATGTGTGTCAGCTAG
 GTAAAGATGACAACTGCCCTGTCTGGCAGTCAGCTTCCAGACAGACTATAGACTATAAAT
 ATGTCCTCATCTGCCTTACCAAGTGTCTTCTTACTACAATGCTGAATGACTGGAAGAAGAA
 CTGATATGGCTAGTTCAGCTAGCTGGTACAGATAATTCAAACCTGCTGTTGGTTTTAATTTT
 GTAACCTGTGGCTGATCTGTAATAAACTTACATTTTCAATAGGTAAAAA

FIGURE 108

CTGCAGGTAGACATCTCCACTGCCAGGAATCACTGAGCGTGCAGACAGCACAGCCTCCTCT
GAAGGCCGCCATACCAGAGTCTGCCTCGGCATGGGCCTCACCATTGAGGCAGCTCCACTG
TCTGTGCTGGTCTGAGGGTGTGCCTGTCAATGGGGGCAGCCATCTCCAGGGGGCCCTCATC
GCCATCGTCTGCAACGGTCTCGTGGGCTTCTTGCTGCTGCTGCTGCTGGGTATCCTCTGCTG
GGCCTGCCATTCTCGTCTGCCGACGTTGACTCTCTCTGAATCCAGTCCCAACTCCAGCCC
TGGCCCCGTGCTGAGAAGGCCCCACCACCCAGAAGCCCAGCCATGAAGGCAGCTACCTGC
TGCAGCCCTGAAGGCCCTGGCCTAGCCTGGAGCCAGGACCTAAGTCCACCTCACCTAGAG
CCTGGAATTAGGATCCAGAGTTCAGCCAGCCTGGGGTCCAGAACTCAAGAGTCCGCCTGCT
TGGAGCTGGACCCAGCGGCCAGAGTCTAGCCAGCTTGGCTCCAATAGGAGCTCAGTGGCCC
TAAGGAGATGGGCCTGGGGTGGGGGCTTATGAGTTGGTGTAGAGCCAGGGCCATCTGGACT
ATGCTCCATCCCAAGGGCCAAGGGTCAGGGGCCGGGTCCACTCTTCCCTAGGCTGAGCACC
TCTAGGCCCTCTAGGTTGGGGAAGCAAACCTGGAACCCATGGCAATAATAGGAGGGTGTCCAG
GCTGGGCCCTCCCTGGTCTCCAGTGTTGCTGGATAATAAATGGAACATATGGCTCTAA
AAAAAAAAAAAAAAAAAA

FIGURE 110

GTTTGAATTCCTTCAACTATACCCACAGTCCAAAAGCAGACTCACTGTGTCCAGGCTACCA
 GTTCTCCAAAGCAAGTCATTTCCCTTATTTAACCGATGTGTCCCTCAAACACCTGAGTGCTA
 CTCCTTATTTGCATCTGTTTTGATAAATGATGTTGACACCCCTCCACCGAATTCCTAAGTGGAA
 TC**ATGT**CGGGAAGAGATACAATCCTTGGCCTGTGTATCCTCGCATTAGCCTTGTCCTTGGCC
 ATGATGTTTACCTTCAGATTATCACCACCCTTCTGGTTCACATTTTCATTTTCATTGGTTAT
 TTTGGGATTGTTGTTTGTCTGCGGTGTTTTATGGTGGCTGTATTATGACTATACCAACGACC
 TCAGCATAGAATTGGACACAGAAAGGGAAAATATGAAGTGCCTGCTGGGGTTTGCATCGTA
 TCCACAGGCATCAGGCAGTGCTGCTCGTCTTGATTTTTGTTCTCAGAAAGAGAATAAAATT
 GACAGTTGAGCTTTTCCAATCACAAATAAGCCATCAGCAGTGCTCCCTTCTGCTGTTCC
 AGCCACTGTGGACATTGCCATCCTCATTTTCTTCTGGGTCCTCTGGGTGGCTGTGCTGCTG
 AGCCTGGGAAGTGCAGGAGCTGCCAGGTTATGGAAGGCGGCCAAGTGAATATAAGCCCTT
 TTCGGGCATTTCGTACATGTGGTGTGATCCATTAAATGGCCTCATCTGGACTAGTGAATCA
 TCCTTGCCTGCCAGCAATGACTATAGCTGGGGCAGTGTTTACTTGTTATTTCACAGAAGT
 AAAAAATGATCCTCCTGATCATCCCATCCTTTCGTCTCTCTCCATTCTCTTCTTCTACCATCA
 AGGAACCGTTGTGAAAGGGTCATTTTTAATCTCTGTGGTGAAGATTCCGAGAATCATTTGCTA
 TGTACATGCAAAACGCACTGAAAGAACAGCAGCATGGTGCATTGTCCAGGTACCTGTTCCGA
 TGCTGCTACTGCTGTTTCTGGTGTCTTGACAAATACCTGCTCCATCTCAACCAGAATGCATA
 TACTACAACCTGCTATTAAATGGGACAGATTTCTGTACATCAGCAAAAGATGCATTCAAAATCT
 TGTCCAAGAAGTCAAGTCACTTTACATCTATTAAGTCTTTGGAGACTTCATAATTTTTCTA
 GGAAAGGTGTTAGTGGTGTGTTTCACTGTTTTTGGAGGACTCATGGCTTTTAACTACAATCG
 GGCATTCCAGGTGTGGGCAGTCCCTCTGTTATTGGTAGCTTTTTTGCCTACTTAGTAGCCC
 ATAGTTTTTTATCTGTGTTTGAAGTGTGCTGGATGCACTTTTCTGTGTTTTGCTGTTGAT
 CTGGAACAAATGATGGATCGTCAGAAAAGCCCTACTTTATGGATCAAGAATTTCTGAGTTT
 CGTAAAAAGGAGCAACAAATTAACAATGCAAGGCACAGCAGGACAAGCACTCATTAAGGA
 ATGAGGAGGGAACAGAAGTCCAGGCCATTGTGAGAT**TAGAT**ATCCCATTTAGTGATCTGTACCT
 GGAAACATTTCTTCTAAGGCCATTACAGAATAGAAGATGAGACCACTAGAGAAAAGTT
 AGTGAATTTTTTTTTTAAAGACCTAATAAACCTATTCTTCTCAAAA

FIGURE 111

MSGRDTILGLCILALALSLAMMFTFRFITTTLLVHIFISLVILGLLFVCGVLWWLYDYDTNDL
SIELDTERENMKCVLGFAlVSTGITAVLLVLIFVLRKRRIKLTVELFQITNKAISSAPFLLFQ
PLWTFAILIFFWVLWVAVLLSLGTAGAAQVMEGGQVEYKPLSGIRYMWSYHLIGLIWTSEFI
LACQOMTIAGAVVTCYFNRSKNDPPDHPILSSLSILFFYHQGTVVKGSFLISVVRIPIVM
YMQNALKEQQHGALSRYLFRCCYCCFWCLDKYLLHLNQNAYTTTAINGTDFCTSAKDAFKIL
SKNSSHFTSINCFGDFIIFLGKVLVVCFTVFGGLMAFNYNRAFQVWAVPLLLVAFFAYLVAH
SFLSVFETVLDALFLCFVDLETNDGSSEKPYFMDQEFLSFVKRSNKLNNARAQQDKHSLRN
EEGTELQAIVR

FIGURE 112

GTTCGATTAGCTCCTCTGAGAAGAAGAGAAAAGTTCTTGGACCTCTCCCTGTTTCTCTCTT
 AGAAATAAATTTGATGGGATTTGTGATGCAGGAAGCCTAAGGGGAAAAAGAAATATTCATTCTG
 TGTGGTGAAAATTTTTTGAIAAAAAAATTCCTTCTTCAAACAAGGGTGTCAATTCTGATATT
TATGAGGACATGTTGTTCTCACATGAAGGCATCTGTTATTGAAATGTTCCCTGTTTGTCTGG
 TGACTGGAGTACATTCAAACAAAGAAACGGCAAGAGATTAAAGGCCCAAGTCTACTGTG
 CCTCAGATCAACTGCGATGTCAAAGCCGGAAGATCATCGATCCGTGAGTTCATTGTGAAATG
 TCCAGCAGGATGCCAGACCCCAAATACCATGTTATGGCACTGACGTGTATCGATCCTACT
 CCAGTGTGTGTGGCGCTGCGGTACACAGTGGTGTGCTTGATAATTCAAGAGGGGAAATACCTT
 GTTCCGAAGGTTGCTGGACAGTCTGGTTACAAAGGGAGTTATTCCAACGGTGTCCAATCGTT
 ATCCCTACCACGATGGAGAGAAATCCTTTATCGTCTTAGAAAGTAAACCCAAAAGGGTGTAAC
 CCTACCCCATCAGTCTTTACATACTCATCATCGAAAAGTCCAGCTGCCCAAGCAGGTGAGACC
 ACAAAGGCTATCAGAGGCCACCTATTCAGGGACAACCTGCACAGCCGGTCACTCTGATGCA
 GCTTCTGGCTGTCACTTAGCTGTGGCCACCCCAACCTTGCAAGGCCATCCCTTCTG
 CTGCTTCTACCACGATCCCCAGACCACAATCAGTGGGCCACAGGAGCCAGGAGATGGAT
 CTCTGGTCCACTGCCACCTACACAAGCAGCCAAAACAGGCCAGAGCTGATCCAGTATCCA
 AAGGCAAGATCCTTCAGGAGCTGCCCTCCAGAAACCTGTTGGAGCGGATGCAGCCTGGGAC
 TTGTTCCAAAGAAAGATTGAGCACACAGTCTTTGGAGCCAGTATCCCTGGGAGATCCAAAC
 TGCAAAATTGACTTGTGCTTTTAATTGATGGGAGCACCAGCATTTGGCAAGCCGGCATCCG
 AATCCGAAGCAGCTCCTGGCTGATGTTGCCCAAGCTCTTGACATTGGCCCTGCCGCTCAC
 TGATGGGTGTGTGTCAGTATGGAGACAACCTGCTACTCATTTAACTCAAGACACACAGC
 AATTCTCGAGATCTGAAGACAGCCATAGAGAAAATTTACTAGAGAGGAGCATTTCTAATGT
 AGGTCGGGCCATCTCCTTTGTGACCAAGAACTCTTTTCCAAAGCCAATGGAAACAGAAGCG
 GGCTCCCAATGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT
 TCAAGACTTGGCAGAGAGTCAAGAAATCAACATTTCTTCATCACCATTGAAGTGTCTGCTGA
 AAATGAGAAGCAGTATGTGGTGGAGCCCACTTTGCAAAACAGGCGCGTGTGCAGAACAAAG
 GCTTCTACTCGCTCCAGCTGCAGAGCTGGTGTGGCCCTCCCAAGACCCCTGCAGCCTTGGTG
 AAGCGGGCTCTGGACACTGACCGCCTGGCCTGCAGCAAGACCTGCTTGAATCGGCTGACAT
 TGGCTTCGTATCGACGGCTCCAGCAGTGTGGGACCGGCAACTTCCGCACCGTCTCTCCAGT
 TTGTGCCAACCTCACAAAGAGTTTGAGATTTCCGACACGGACAGCCGATCGGGGGCGTG
 CAGTACACCTACGAACAGCGGCTGGAAGTTGGGTTCGACAAGTACAGCAGCAAGCCTGACAT
 CCTCAACGCCATCAAGAGGGTGGGCTACTGGAGTGGTGGCACCAGCAGCGGGGCTGCCATCA
 ACTTCGCCCTGGAGCAGCTCTTCAAGAAGTCCAGGCCAACAAAGAGGAAGTTAATGATCCTC
 ATCACCGACGGGAGGTCCTACGACGACGTCGGGATCCAGCCATGGCTGCCATCTGAAGGG
 AGTGATACCTATGCGATAGGCGTTGCCCTGGGCTGCCAAGAGGAGCTAGAAGTCAATGGCA
 CTCACCCGCCAGAGACCACTCCTTCTTGTGGACGAGTTTGACAACCTCCATCAGTATGTC
 CCCAGGATCATCCAGAACTTTGTACAGAGTCAACTCACAGCCTCGGAAC**TGA**ATTCAAG
 CAGGCAAGAGCACCAGCAAGTGTCTGCTTTACTAACTGACGTGTGGACCAACCCACCGCTTAA
 TGGGCGACGCACCGTGATCAAGTCTTGGGCGAGGCATGGAGAAACAAATGCTTGTATTATA
 TTCTTTGGCATCATGCTTTTTCATATTCAAAACCTGGAGTTACAAAGATGATCACAAACGT
 ATAGAATTAGGCCAAAGGCTACATCATGTTGAGGGTGTGGAGATTTTACATTTGACAATT
 GTGATCAATGTAGGAATTGCTGAATTAATGTTTGAAGGATGAAAGTAAAAAATAAAAAA
 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA
 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA
 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA

FIGURE 113

MRTVVLTMKASVIEMFLVLLVTVGVHSNKETAKKIKRPKFTVPQINCVDKAGKIIDPEFIVKC
PAGCQDPKYHVYGTDTVYASYSSVCGAAVHSGVLDNSGGKILVRKVAGQSGYKGSYNGVQSL
SLPRWRESFIVLESKPKKGVTPSALTYSKSPAAQAGETTKAYQRPPIPGTTAQPVTLMO
LLAVTVAVATPTTLPRPSPSAASTTSIPRPQSVGHRSEQEMDLWSTATYTSSQNRPRADPGIQ
RQDPGAAAFQKPVGADVSLGLVPKEELSTQSLEPVSLGDPNCKIDLSFLIDGSTSIGKRRFR
IQKQLLADVAQALDIGPAGPLMGVVQYGDNPATFNKTHTNRDCLKTAIEKITQRGGLSNV
GRAISFVTKNFFSKANGNRSGAPNVVVVMVDGWPTDKVEEASRLARESGINIFFITIEGAAE
NEKQYVVEPNFANKAVCRTNGFYSLHVQSWFGLHKTLPVLRVCDTDRLACSKTCLNSADI
GFVIDGSSSVGTGNFRTVLQFVTNLTKEFEISDTRIGAVQYTYEQRLFEFGFDKYSSKPDIL
LNAIKRVGYWGGTSTGAAINFALEQLFKKSKPNKRKLMILITDGRSYDDVRIPAMAAHLKG
VITYAIGVAWAAQEELEVIATHPARDHSEFFVDEFNLHQYVPRIIQNICTEFNSQPRN

FIGURE 114

CAGGATGAACTGGTTGCAGTGGCTGCTGCTGCTGCGGGGCGCTGAGAGGACACGAGCTCTA
TGCCTTTCCGGCTGCTCATCCCGCTCGGCCTCCTGTGCGCGCTGCTGCCTCAGCACCATGGT
 GCGCCAGGTCCCGACGGCTCCGCGCCAGATCCCGCCCACTACAGTTTTTCTCTGACTCTAAT
 TGATGCACTGGACACCTTGCTGATTTTGGGGAATGTCTCAGAATTCCAAAGAGTGGTTGAAG
 TGCTCCAGGACAGCGTGGACTTTGATATGTAGTGAACGCCTCTGTGTTTGAACAAACATT
 CGAGTGGTAGGAGGACTCCTGTCTGCTCATCTGCTCTCCAAGAAGGCTGGGGTGGAAGTAGA
 GGCTGGATGGCCCTGTTCCGGGCCTCTCCTGAGAATGGCTGAGGAGGCGGCCGAAAACCTC
 TCCAGCCTTTAGACCCCCACTGGCATGCCATATGGAACAGTGAACCTACTTCATGGCGTG
 AACCCAGGAGAGACCCCTGTACCTGTACGGCAGGGATTGGGACCTTCATTGTTGAATTTGC
 CACCTTGAGCAGCCTCACTGGTGACCCGGTGTTCGAAGATGTGGCCAGAGTGGCTTTGATGC
 GCCTCTGGGAGAGCCGGTCAGATATCGGGCTGGTCGGCAACCACATTGATGTGCTCACTGGC
 AAGTGGGTGGCCAGGACGCAAGGATCGGGGCTGGCGTGGACTCCTACTTTGAGTACTTGGT
 GAAAGGAGCCATCCTGCTTCAGGATAAGAAGCTCATGGCCATGTTCTAGAGTATAACAAAG
 CCATCCGGAACACACCCGCTTCGATGACTGGTACCTGTGGGTTCCAGATGTACAAGGGGACT
 GTGTPCATGCCAGTCTTCCAGTCCCTTGAGAGCCTACTGGCCTGGTCTTCAGAGCCTCATTTGG
 AGACATTGACAATGCCATGAGGACCTTCCTCAACTACTACACTGTATGGAAGCAGTTTGGGG
 GGCTCCCGAATTCTACAACATTCCTCAGGGATACACAGTGGAGAAGCGAGAGGGCTACCCA
 CTTTCGGCCAGAACTTATTGAAAGCGCAATGTACCTCTACCGTGCCACGGGGGATCCCACCTT
 CCTAGAACTCGGAAGAGATGCTGTGGAATCCATTGAAAAAATCAGCAAGGTGGAGTGGCGAT
 TTGCAACAATCAAAGATCTGCGAGACCACAAGCTGGACAACCGCATGGAGTCGTTCTCTCTG
 GCCGAGACTGTGAAATACCTCTACCTCCTGTTTGACCCAACCAACTTCATCCACAACAATGG
 GTCCACCTTCGACGCGGTGATCACCCCTATGGGGAGTGCATCCTGGGGGCTGGGGGGTACA
 TCTTCAACACAGAAGCTCACCCATCGACCTTGCCGCCCTGCACTGCTGCCAGAGGCTGAAG
 GAAGAGCAGTGGGAGTGGAGGACTTGATGAGGGAATTCTACTCTCTCAAACGAGCAGGTC
 GAAATTTAGAAAAACACTGTTAGTTTCGGGGCCATGGGAACCTCCAGCAAGGCCAGGAACAC
 TCTTCTCACCAGAAAACCATGACCAAGGCAAGGAGAGGAAGCCTGCCAAACAGAAAGGTCCCA
 CTTCCTCAGCTGCCCCAGTCAGCCCTTCACCTCCAAGTTGGCATTACTGGGACAGGTTTTCTT
 AGACTCCTCA**TAA**CCACTGGATAATTTTTTTATTTTTATTTTTTTGAGGCTAAACTATAATA
 AATTGCTTTTGGCTATCATAAAA

FIGURE 115

MPFRLLIPLGLLCALLPQHHGAPGPDGSAPDPAHYSFSLTLIDALDTLLILGNVSEFQRVVE
VLQDSVDFDIDVNASVFETNIRVVGGLLSAHLLSKKAGVEVEAGWPCSGPLLRMAEEAARKL
LPAFQTPTGMPYGTVNLLHGVNPGETPVTCTAGIGTFIVEFATLSSLTGDPVFEDVARVALM
RLWESRSDIGLVGNHIDVLTGKWVAQDAGIGAGVDSYFEYLVKGAILLQDKKLMAMFLEYNK
AIRNYTRFDDWYLVWQMYKGTVSMFVFQSLEAYWPGQLSLIGDIDNAMRTFLNYYTVWKQFG
GLPEFYNIPOGYTVEKREGYPLRPELIESAMYLYRATGDPITLLEGRDAVESIEKISKVECG
FATIKDLRDHKLDRMESFFLAETVKYLYLLFDPTNFIHNNGSTFDAVITPYGECILGAGGY
IFNTEAHPIDLAALHCCQRLKEEQWEVEDLMREFYSLKRSRKFQKNTVSSGPEPPARPGT
LFSPENHDQARERKPAKQKVPLLSCPSQPFTSKLALLGQVFLDSS

FIGURE 116

AAAGTTACATTTTCTCTGGAAGTCTCCTAGGCCACTCCCTGCTGATGCAACATCTGGGTTTG
 GGCAGAAAAGGAGGTGCTTCGGAGCCCGCCCTTTCTGAGCTTCTGGGCCGGCTCTAGAACA
 ATTCAAGGCTTCGCTGCGACTCAGACCTCAGCTCCAACATATGCATTCTGAAGAAAGATGGCT
 GAGATGGACAGAATGCTTTATTTTGGAAAGAAACAATGTTCTAGGTCAAACCTGAGTCTACCA
AATGCAGACTTTTACAATGGTTCTAGAAAGAACTGGACAAGTCTTTTCATGTGGTTTTTCT
 ACGCATTTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGCCTGCCCTCAGAACCTC
 TCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCAGTGATCGCGCTGGAGA
 AACAGTGTACTATTCTGTGCAATACCAGGGGGAGTACGAGAGCCTGTACACGAGCCACATCT
 GGATCCCCAGCAGCTGGTGCTCACTCACTGAAGGTCTGAGTGTGATGTCACTGATGACATC
 ACGGCCACTGTGCCATACAACCTTCGTGTGAGGCCACATTGGGCTCACAGACCTCAGCCTG
 GAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTACCCGACCTGGGATGGAGA
 TCACCAAAGATGGCTTCCACCTGGTTATGAGCTGGAGGACCTGGGGCCCCAGTTTGAGTTC
 CTTGTGGCCTACTGGAGGAGGGAGCCTGGTGCCGAGGAACATGTCAAATGGTGAGGAGTGG
 GGGTATTCCAGTGCACCTAGAAACCATGGAGCCAGGGGCTGCATACTGTGTGAAGGCCAGA
 CATTCGTGAAGGCCATTGGGAGGTACAGCGCCTTCAGCCAGACAGAATGTGTGGAGGTGCAA
 GGAGAGGCCATTCCCCTGGTACTGGCCCTGTTTGCCCTTTGTTGGCTTCATGCTGATCCTTGT
 GGTCTGCCACTGTTCTGTGGAATAAGGCGGCTGCTCCAGTACTCCTGTTGCCCGCTGG
 TGGTCTCTCCAGACACCTTGAAATAACCAATTACCCAGAAAGTTAATCAGCTGCAGAAGG
 GAGGAGGTGGATGCCTGTGCCACGGCTGTGATGTCCTGAGGAACTCCTCAGGGCCTGGAT
 CTCAT**TAG**GTTTGCGAAGGGCCAGGTGAAGCCGAGAACCTGGTCTGCATGACATGGAACC
 ATGAGGGGACAAGTTGTGTTTCTGTTTTCCGCCACGGACAAGGGATGAGAGAAGTAGGAAGA
 GCCTGTTGTCTACAAGTCTAGAAGCAACCATCAGAGGCAGGGTGGTTTGTCTAACAGAACAC
 TGACTGAGGCTTAGGGGATGTGACCTCTAGACTGGGGCTGCCACTTGTGCTGAGCAACC
 CTGGGAAAAGTGACTTATCCCTTCGGTCCCTAAGTTTCTCATCTGTAATGGGGGAATTACC
 TACACACCTGCTAAACACACACACAGAGTCTCTCTATATATACACAGTACACATAAA
 TACACCCAGCACTTGCAAGGCTAGAGGGAACCTGGTGACACTCTACAGTCTGACTGATTGAG
 TGTCTCTGGAGAGCAGGACATAAATGTATGATGAGAATGATCAAGGACTCTACACACTGGGT
 GGCTTGGAGAGCCCACTTTCACAGAATAATCCTTGAGAGAAAAGGAATCATGGGAGCAATGG
 TGTGAGTTCACTTCAAGCCCAATGCCGGTGAGAGGGGAATGGCTTAGCGAGCTCTACAGT
 AGGTGACCTGGAGGAAGGTACAGCCACACTGAAAATGGGATGTGCATGAACACGGAGGATC
 CATGAACACTGTAAAGTGTGACAGTGTGTGCACACTGCAGACAGCAGGTGAAATGTATGT
 GTGCAATGCGACGAGAATGCAGAAGTCACTAACATGTGCATGTTTGTGTGCTCCTTTTTTC
 TGTGGTAAAGTACAGAATTACAGCAATAAAAGGGCCACCCTGGCCAAAAGCGGTAAAAAA
 AAAAAAAAAA

FIGURE 117

MQTFTMVLEEIIWTSLFMWWFFYALIPCLLTDEVAILPAPQNLSVLSTNMKHLMLWSPVIAIGE
 TVYYSVEYQGEYESLYTSHIWIPSSWCSLTEGPECDDVTDITATVPYNLRVRATLGSQTS
 SILKHFFNRRNSTILTRPGMEITKDGFLVIELEDLGPQFEFLVAYWRREPGAEEHVKMVRSG
 GIPVHLETMEPGAAYCVKAQTFVKAIGRYSAFSQTECVQGEAIPLVLALFAFVGFMILILV
 VVPLFVWKMGRLLQYSCCPVVVLPDTLKITNSPQKLISCRREEVDACATAVMSPEELLRAWIS

Important features:**Signal peptide:**

amino acids 1-29

Transmembrane domain:

amino acids 230-255

N-glycosylation sites.

amino acids 40-43 and 134-137

Tissue factor proteins homology.

amino acids 92-119

Integrins alpha chain protein homology.

amino acids 232-262

FIGURE 118

TCCTGCTGATGCACATCTGGGTTTGGCAAAGGAGGTTGCTTCGAGCCGCCCTTTCTAGCTT
 CCTGGCCGGCTCTAGAACAATTCAGGCTTCGCTGCGACTAGACCTCAGCTCCAACATATGCA
 TTCTGAAGAAAGATGGCTGAGATGACAGAATGCTTTATTTTGGAAAGAAACAATGTCTAGG
 TCAAACCTGAGTCTACCAAATGCAGACTTTCACAATGGTTCTAGAAGAAATCTGGACAAGTCT
 TTTTCATGTGGTTTTTCTACGCATTGATTCCATGTTTGCTCACAGATGAAGTGGCCATTCTGC
 CTGCCCTCAGAACCTCTCTGTACTCTCAACCAACATGAAGCATCTCTTGATGTGGAGCCCA
 GTGATCGCGCCTGGAGAAACAGTGTACTATTCTGTGCAATAACAGGGGGAGTACGAGAGCCT
 GTACACGAGCCACATCTGGATCCCAGCAGCTGGTGCTCACTCACTGAAGGTCCTGAGTGTG
 ATGTCACTGATGACATCACGGCCACTGTGCCATACAACCTTTGTGTCAGGGCCACATTGGGC
 TCACAGACCTCAGCCTGGAGCATCCTGAAGCATCCCTTTAATAGAACTCAACCATCCTTAC
 CCGACCTGGGATGGAGATCACCAAAGATGGCTTNCACCTGGTTATTGAGCTGGAGGACCTGG
 GGCCCCAGTTTGAGTTCCTTGTGGCCTANTGGAGGAGGGGCGCAACCCCTTGCGGCCAAGGG
 GTTNGCGAACCCTTGCGGCCGCTGGGGTATCTCTCGAGAAAAGAGAGGCCCAATATGACCCAC
 ATACTCAATATGGACGAANTGCTATTGTCCACCTGTTTGAGTGGCGCTGGGTTGAT

FIGURE 119

CGGACGCGTGGGCCGCCACCTCCGGAACAAGCC**ATG**GTGGCGGCGACGGTGGCAGCGCGCTG
GCTGCTCCTGTGGGCTGCGGCCTGCGCGCAGCAGGAGCAGGACTTCTACGACTTCAAGCGCG
TCAACATCCGGGGCAAACCTGGTGTGCTGCGTGGAGAAGTACCGCGGATCGGTGTCCCTGGTGGTG
AATGTGGCCAGCGAGTGCGGCTTCACAGACCAGCACTACCGAGCCCTGCAGCAGCTGCAGCG
AGACCTGGGCCCCCACCACCTTTAACGTGCTCGCCTTCCCCTGCAACCAGTTTGGCCAACAGG
AGCCTGACAGCAACAAGGAGATTGAGAGCTTTGCCCGCCGACCTACAGTGTCTCATTTCCC
ATGTTTAGCAAGATTGCAGTCACCGGTACTGGTGCCCATCCTGCCTTCAAGTACCTGGCCCA
GACTTCTGGGAAGGAGCCCACCTGGAACCTTCTGGAAGTACCTAGTAGCCCCAGATGGAAGG
TGGTAGGGGCTTGGGACCCAACTGTGTGTCAGTGGAGGAGTGCAGACCCAGATCACAGCGCTC
GTGAGGAAGCTCATCTACTGAAGCGAGAAGACTT**TAA**CCACCGCGTCTCCTCCTCCACCA
CCTCATCCCGCCCACCTGTGTGGGCTGACCAATGCAAACCTCAAATGGTGTCTCAAAGGGAG
AGACCCACTGACTCTCCTTCTCTTACTCTTATGCCATTGGTCCCATCATTCTTGTGGGGGAA
AAATTCTAGTATTTTGATTATTTGAATCTTACAGCAACAAATAGGAACCTCTGGCCAATGAG
AGCTCTTGACCAAGTGAATCACCAGCCGATACGAACGTCTTGCCAACAAAAATGTGTGGCAAA
TAGAAGTATATCAAGCAATAATCTCCACCCAAAGGCTTCTGTAAACTGGGACCAATGATTAC
CTCATAGGGCTGTGTGAGGATTAGGATGAAATACCTGTGAAAGTGCCTAGGCAGTGCCAGC
CAAATAGGAGGCATTCAATGAACATTTTTGCATATAAACCAAAAAATAACTTGTATCAAT
AAAAACTTGCATCCAACATGAATTTCCAGCCGATGATAATCCAGGCCAAAGGTTTAGTTGTT
GTTATTTCTCTGTATATTATTCTTCATTACAAAAGAAATGCAAGTTTATTGTAACAATCCA
AACAAATACCTCACGATATAAAATAAAATGAAAGTATCCTCCTCAAAA

FIGURE 121

CGGACGCGTGGGCGGGCCGGGACGCAGGGCAAAGCGAGGCC**ATG**GTGCTCTACGTGGGATGC
 TGGCCCTGGGGAGGCTGTGCGCCGGGAGCTCGGGGGTGCTGGGGGCCGGGCCGCCCTCTCT
 CGGAGTTGGCAGGAAGCCAGGTTGCAGGGTGTCCGCTTCCTCAGTTCAGAGAGAGGTGGATCG
 CATGTCTCCACGCCCATCGGAGGCCCTCAGCTACGTTCAAGGGGTGCACCAAAAGCATCTTA
 ACAGCAAGACTGTGGCCAGTGCCTGGAGACCACAGCACAGAGGGTCCCAGAACGAGAGGCC
 TTGGTTCGTCTCCATGAAGACGTCAAGTTGACCTTTGCCCAACTCAAGGAGGAGGTGGACAA
 AGCTGCTTCTGGCCTCCTGAGCATTGGCCTCTGCAAAGGTGACCGGCTGGGCATGTGGGGAC
 CTAATCTCTATGCATGGGTGCTCATGCAGTTGGCCACCGCCAGGCGGGCATCATTCTGGTG
 TCTGTGAACCCAGCCTACCAGGCTATGGAAGTGGAGTATGTCCTCAAGAAGGTGGGCTGCAA
 GGCCCTTGTTTCCCCAAGCAATTCAAGACCCAGCAATACTACAAGCTCCTGAAGCAGATCT
 GTCCAGAAGTGGAGAATGCCAGCCAGGGGCCCTTGAAGAGTCAGAGGCTCCAGATCTGACC
 ACAGTCATCTCGGTGGATGCCCTTTGCGGGGACCCCTGCTCCTGGATGAAGTGGTGGCGGC
 TGGCAGCACACGGCAGCATCTGGACCAGTCCAATACAACCAGCAGTTCTCTGTCTGCCATG
 ACCCATCAACATCCAGTTCACTCGGGGACAAACAGGCAGCCCCAAGGGGGCCACCTCTCC
 CACTACAACATTGTCAACAACCTCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGAC
 ACCAGAGCAGTTGCGGATGATCCTGCCCAACCCCTGTACCATTTGCCTGGGTTCCGTGGCAG
 GCACAATGATGTCTGATGTACGGTGCCACCCTCATCTGGCCTCTCCATCTTCAATGGC
 AAGAAGGCATCGGAGGCCATCAGCAGAGAGAGAGGCCACCTTCCTGTATGGTACCCCCACGAT
 GTTCTGGACATTCTGAACAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAG
 GTGTCTATGTCTGGTCCCCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAAT
 ATGAAGGACTGGTGGTTGCTTATGGAACACAGAGAACAGTCCCGTGACATTGCGCACTT
 CCCTGAGGACACTGTGGAGCAGAAGGCAGAAAGCGTGGGCAGAAATATGCCTCACACGGAGG
 CCCGATCATGAACATGGAGGCAGGACGCTGGCAAAGCTGAACACGCCCGGGGAGCTGTGC
 ATCCGAGGGTACTGCGTCATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGT
 GGATCAGGACAAGTGGTATTGGACAGGAGATGTGCCCAATGAATGAGCAGGGCTTCTGCA
 AGATCGTGGGCCGCTCTAAGGATATGATCATCCGGGTGGTGAGAACATCTACCCCGCAGAG
 CTCGAGGACTTCTTTCACACACACCCGAAGGTGCAGGAAGTGCAGGTGGTGGGAGTGAAGGA
 CGATCGGATGGGGGAAGAGATTTGTGCCTGCATTGCGCTGAAGGACGGGGAGGAGACCACGG
 TGGAGGAGATAAAAGCTTTCTGCAAAGGGAAGATCTCTCACTTCAAGATTCCGAAGTACATC
 GTGTTTGTACAAACTACCCCTCACCAATTTTCAGGAAAGATCCAGAAATTCAACTTCGAGA
 GCAGATGGAAACGACATCTAAATCTCT**TGA**AATAAAGCAGCAGGCCTGCTGGCCGGTTGGCTT
 GACTCTCTCTGTGAGAAATGCAACCTGGCTTTATGCACCTAGATGTCCCCAGCACCAGGCTTC
 TGAGCCAGGCACATCAATGTGCAAGGAATTGACTGAACCACTAAGACTCCTGGATGGGTG
 CGGGAAGTCGCTGGGCACAAGGTGCCAAAGGCAGGCAGCCTGCCAGGCCCTCCCTCCTG
 TCCATCCCCCACATTCCCTCTGTCTCTTGTGATTTGGCATAAAGAGCTTCTGTTTTCTTT
 GAAAAAAAAAAAAAAAAA

FIGURE 122

MAVYVGLRLRLGRLCAGSSGVLGARAALSRWQEARLQGVRFLLSSREVD RMVSTPIGGLSYVQ
 GCTKKHLNSKTVGQCLETТАQRVPEREALVVLHEDVRLTFAQLKEEVDKAASGLLSIGLCKG
 DRLGMWGPNSYAWVLMQLATAQAGIILVSVNPAYQAMELEYVLKKVGCKALVF PKQFKTQQY
 YNVLKQICPEVENAQPGALKSQRLPDLTTVISVDAPLPGTLLLDEVVAAGSTRQHLDQLQYN
 QQFLSCHDPINIQTSGTTGSPKGATLSHYNIVNNSNILGERLKLHEKTPEQLRMILPNPLY
 HCLGSVAGTMCLMYGATLILASPIFNGKKALEAISRERGTFLYGTPTMFVDILNQPDFSSY
 DISTMCGGVIAGSPAPPELIRAIINKINMKDLVVAYGTTENSPTVFAHFPEDTVEQKAESVG
 RIMPHTEARIMNMEAGTLAKLNTPGELCIRGYCVMLGYWGEPQKTEEAVDQDKWYWTGDVAT
 MNEQGFCIKIVGRSKDMIIRGENIYPAELEDFHHTHPKVQEVQVVGKDDRMGEEICACIRL
 KDGEETTVEEIKAFCKGKISHFKIPKYIVFVTNYPLTISGKIQKFKLREQMERHLNL

Signal Peptide:

amino acids 1-22

Transmembrane Domains:

amino acids 140-161, 213-229, 312-334

Putative AMP-binding Domain Signature:

amino acids 260-271

N-myristoylation Sites:

amino acids 19-24, 22-27, 120-125, 203-208, 268-273, 272-277,
 314-319, 318-323, 379-384, 380-385, 409-413

N-glycosylation Site:

amino acids 282-285

FIGURE 123

CAACTCCAACATTTTAGGAGAGCGCCTGAAACTGCATGAGAAGACACCAGAGCAGTTGCGGA
TGATCCTGCCCAACCCCTGTACCATTGCCTGGGTTCGGTGCCAGGCACAATGATGTGTCTG
ATGTACGGTGCCACCCTCATCCTGGCCTCTCCCATCTTCAATGGCAAGAAGGCACCTGGAGGC
CATCAGCAGAGAGAGAGGCACCTTCCTGTATGGTACCCACGATGTTCTGGACATTCTGA
ACCAGCCAGACTTCTCCAGTTATGACATCTCGACCATGTGTGGAGGTGTCATTGCTGGGTCC
CCTGCACCTCCAGAGTTGATCCGAGCCATCATCAACAAGATAAATATGAAGGACCTGGTGGT
TGCTTATGGAACCACAGAGAACAGTCCCGTGACATTTCGCGCACCTCCCTGAGGACACTGTGG
AGCAGAAGGCAGAAAGCGTGGGCAGAATTATGCCTCACACGGAGGCGCGGATCATGAACATG
GAGGCAGGGACGCTGGCAAAGCTGAACACGCCCGGGAGCTGTGCATCCGAGGGTACTGCGT
CATGCTGGGCTACTGGGGTGAGCCTCAGAAGACAGAGGAAGCAGTGGATCAGGACAAGTGGT
ATTGGACAGGAGATGTCGCCAC

FIGURE 124

GAGCAGGACGGAGGCC**ATG**GACCCCGCCAGGAAAGCAGGTGCCCAGGCCATGATCTGGACTGC
 AGGCTGGCTGCTGCTGCTGCTGCTTCGCGGAGGAGCGCAGGCCCTGGAGTGCTACAGCTGCG
 TGCAGAAAGCAGATGACGGATGCTCCCCGAACAAGATGAAGACAGTGAAGTGCGCGCCGGGC
 GTGGACGTCTGCACCGAGGCCGTGGGGCGGTGGAGACCATCCACGGACAATTTCTCGCTGGC
 AGTGCGGGGTGCGGTTTCGGGACTCCCCGGCAAGAATGACCGCGGCCTGGATCTTCACGGGC
 TTCTGGCGTTTCATCCAGCTGCAGCAATGCGCTCAGGATCGCTGCAACGCCAAGCTCAACCTC
 ACCTCGCGGGCGCTCGACCCGGCAGGTAATGAGAGTGATACCCGCCAACGGCGTGGAGTG
 CTACAGCTGTGTGGGCTGAGCCGGGAGGCGTGCCAGGGTACATCGCCGCCGGTCTGAGAGCT
 GCTACAACGCCAGCGATCATGTCTACAAGGGCTGCTTCGACGGCAACGTCACTTTGACGGCA
 GCTAATGTGACTGTGTCTTGCCTGTCCGGGGCTGTGTCCAGGATGAATTCTGCACTCGGGA
 TGGAGTAACAGGCCCAGGGTTTCACGCTCAGTGGCTCCTGTGTCAGGGGTCCCGCTGTAAC
 CTGACCTCCGCAACAAGACCTACTTCTCCCTCGAATCCACCCCTTTGTCGGGCTGCCCCCT
 CCAGAGCCCACGACTGTGGCCTCAACCACATCTGTACCACCTTCTACCTCGGCCCCAGTGAG
 ACCACATCCACCACCAAAACCCATGCCAGCGCCAACAGTCAGACTCCGAGACAGGGAGTAG
 AACACGAGGCCTCCGGGATGAGGAGCCAGGTTGACTGGAGGCGCGCTGGCCACCAGGAC
 CGCAGCAATTGAGGCGAGTATCCTGCAAAAGGGGGGGCCAGCAGCCCCATAATAAAGGCTG
 TGTGGCTCCACAGCTGGATTGGCAGCCCTTCTGTTGGCCGTGGCTGCTGGTGTCTACTG**T**
GAGCTTCTCCACCTGGAAATTTCCCTCTCACCTACTTCTCTGGCCCTGGGTACCCCTCTTCT
 CATCACTTCTCTGTTCCACCACTGGACTGGGCTGGCCAGCCCTGTTTTTCCAACATTCCC
 CAGTATCCCCAGCTTCTGCTGCGCTGGTTTGGCGCTTGGGAAATAAAATACCGTGTATAT
 ATTCTGCCAGGGGTGTTCTAGCTTTTTGAGGACAGCTCCTGTATCCTTCTCATCCTTGTCTC
 TCCGCTTGTCTCTTGTGATGTTAGGACAGAGTGAGAGAAGTCAGCTGTACGGGGAAGGTG
 AGAGAGAGGATGCTAAGCTTCCTACTCACTTTCTCCTAGCCAGCCTGGACTTTGGAGCGTGG
 GGTGGGTGGGACAATGGCTCCCCACTCTAAGCACTGCCTCCCCTACTCCCGCATCTTTGGG
 GAATCGGTTCCCATATGTCTTCTTACTAGACTGTGAGCTCCTCGAGGGGGGGCCCGGTAC
 CCAATTGCGCCCTATAGTGAGTCGTA

FIGURE 125

MDPARKAGAQAMIWTAGWLLLLLLRGGAQALECYSCVQKADDGCS PNKMKT VKCAPGVDVCT
EAVGAVETIHGQFSLAVRGCGSGLPGKNDRGLDLHGLLAFIQLQQCAQDRCNAKLNLTSRAL
DPAGNESAYPPNGVECYSCVGLSREACQGTSPFVVCYNASDHVYKGC FDGNVTLTAANVTV
SLPVRGCVQDEFCTRDGVTGPGFTLSGSCCQGSRCNSDLRNKTYFSPRIPLVRLPPPEPTT
VASTTSVTTST SAPVRPTSTTKPMPAPTSQTPRQGEHEASRDEEPRLTGGAAGHQDRSNSG
QYPKGGPQQPHNKGCVAPTAGLAALLLAVAAGVLL



FIGURE 126

[illegible]

127/330

FIGURE 127

MELVLVFLCSLLAPMVLASAAEKEKEMDPFHYDYQTLRIGGLVFAVVLFSVGILLILSRCK
CSFNQKPAPGDEEAQVENLITANATEPQKQRTevQPSGGSLWNLRRLEPLDANVDA

127/330

FIGURE 128

AAACTTGACGCCATGAAAGATCCC GGTCCTTCCTGCCGTGGTGCTCCTCTCCCTCCTGGTGCT
 CCACCTCTGCCCAGGGAGCCACCCTGGGTGGTCCTGAGGAAGAAAGCACCATTTGAGAATTATG
 CGTCACGACCCGAGGCCCTTTAACACCCCGTTCTCTGAACATCGACAAATTGCGATCTGCGTTT
 AAGGCTGATGAGTTCCTGAACTGGCACGCCCTCTTTGAGTCTATCAAAGGAAACTTCCTTT
 CCTCAACTGGGATGCCTTTCCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCCAGT
GACCATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGCTGATTCTCAACCTACCATAACT
 CTTTCCTGCCTCAGGAACTCCAATAAAACATTTTCCATCCAAA



MKIPVLPVVLSSLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSFAKADE
 FLNWHALFESIKRKLFLNWDAFPCLKGLRSATPDAQ

FIGURE 130

CAGTTCTGAAATCAATGGAGTTAATTTAGGGAATACAAACCAGCCATGGGGGTGGAGATTGC
CTTTGCCTCAGTGATTCTCACCTGCCTCTCCCTTCTGGCAGCAGGAGTCTCCCAGGTTGTTC
TTCTCCAGCCAGTTCCAACCTCAGGAGACAGGTCCCAAGGCCATGGGAGATCTCTCCTGTGGC
TTTGCCGGCCACTCATGAGAGTGTTTTTTGTGTAAAGTATTTTTAGAATACTGTTGACTTCT
TCATGATTTAATAACCATCCTTTGCGAAGTTTTATGAGGCTTTAGGGGAATGTCAACCCTCA
AATTTTTGTTATACTAGATGGCTTCCATTTACCCACCACTATTTTAAGGTCCCTTTATTTTT
AGGTTCAAGGTTCAATTGACTTGAGAAAGTGCCTTCTGCAGCTTCATTGATTTTGTTTATC
TTCATAATTAATTGTAACGATTAAAAAGAATAAGAGCACGCAGACCTCTAGGAGAATATTT
TATCCCTGGGTGCCCCTGACACATTTATGTAGTGATCCCAAAATGTGATTGTTAATTTAAA
TGTTATTCTAATATTAGTACATTCAGTTGTGATGTAATATGAATAACCAGAATCTATTTCTT
AAAAGTTTTGAGTATATTTTTCAACTAGATATTTGTATAGAAAGACTGAATAGTGATG

131/330

FIGURE 131

MGVEIAFASVILTCLSLLAAGVSQVLLQPVPTQETGPKAMGDLSCGFAGHS

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FIGURE 132

GGGGAATCTGCAGTAGGCTCTGCCGGCC**ATG**GAGTGGTGGGCTAGCTCGCCGCTTCGGCTCTG
 GCTGCTGTTGTTCCCTCCTGCCCTCAGCGCAGGGCCGCCAGAAGGAGTCAGGTTCAAATGGA
 AAGTATTTATTGACCAAATTAACAGGTCCTTTGGAGAATTACGAACCATGTTCAAGTCAAAC
 TGCAGCTGCTACCATGGTGTCTATAGAAGAGGATCTAACTCCTTTCCGAGGAGGCATCTCCAG
 GAAGATGATGGCAGAGGTAGTCAGACGGAAGCTAGGGACCCACTATCAGATCACTAAGAACA
 GACTGTACCGGGAAAATGACTGCATGTTCCCTCAAGGTGTAGTGGTGTGAGCACTTTATT
 TTGGAAGTGATCGGGCGTCTCCCTGACATGGAGATGGTGATCAATGTACGAGATTATCTCA
 GGTTCCTAAATGGATGGAGCCTGCCATCCAGTCTTCTCCTTCAGTAAGACATCAGAGTACC
 ATGATATCATGTATCCTGCTTGGACATTTTGGGAAGGGGACCTGCTGTTTGGCCAATTTAT
 CCTACAGTCTTGGACGGTGGACCTCTTCAGAGAAGATCTGGTAAGGTCAGCAGCACAGTG
 GCCATGGA AAAAGAAA AACTCTACAGCATATTTCCGAGGATCAAGGACAAGTCCAGAACGAG
 ATCCTCTCATTTCTTCTGTCTCGAAAAACCCAAAACCTGTTGATGCAGAATACACCAAAAAC
 CAGGCTTGAAAATCTATGAAAGATACCTTAGGAAAGCCAGCTGCTAAGGATGTCCATCTTGT
 GGATCACTGCAATACAAAGTATCTGTTTAATTTTCGAGGCGTAGCTGCAAGTTTCCGGTTTA
 AACACCTCTTCTGTGTGGCTCACTTGTTTTCCATGTTGGTGATGAGTGGCTAGAATCTTTC
 TATCCACAGCTGAAGCCATGGGTTCACTATATCCAGTCAAAACAGATCTCTCCAATGTCCA
 AGAGCTGTTACAATTTGTAAAAGCAAATGATGATGTAGCTCAAGAGATTGCTGAAAGGGGAA
 GCCAGTTTATTAGGAACCATTTGCAGATGGATGACATCACCTGTTACTGGGAGAACCTCTTG
 AGTGAATACTCTAAATCCTGTCTTATAATGTAACGAGAAGGAAAGGTTATGATCAAATTAT
 TCCCAAAATGTTGAAAACCTGAAC**TAG**TAGTCATCATAGACCATAGTCCTCTTTGTGGCA
 ACAGATCTCAGATATCCTACGGTGAGAAGCTTACCATAAGCTTGGCTCCTATACCTTGAATA
 TCTGCTATCAAGCCAATACCTGGTTTTCTTATCATGCTGCACCCAGAGCAACTCTTGAGA
 AAGATTTAAATGTGTCTAATACTGATATGAAGCAGTTCAACTTTTTGGATGAATAAGGA
 CCAGAAATCGTGAGATGTGGATTTTGAACCAACTCTACCTTTTCAATTTTCTTAAGACCAATC
 ACAGCTTGTGCCCTCAGATCATCCACCTGTGTGAGTCCATCACTGTGAAATTGACTGTGTCCA
 TGTGATGATGCCCTTTGTCCATTATTTGGAGCAGAAAATTCGTCAATTGGAAGTAGTACAA
 CTCATTGCTGGAATTGTGAAATTATTCAAGGCGTGATCTCTGTCACTTTATTTTAAATGTAGG
 AAACCTATGGGGTTTATGAAAAAATACTTGGGGATCATCTCTGAATGGTCTAAGGAAGCGG
 TAGCCATGCCATGCAATGATGTAGGAGTTCTCTTTTGTAAACCAATAAACTCTGTTACTCAG
 GAGGTTTCTATAATGCCACATAGAAAGAGGCCAATGCATGAGTAATTATTGCAATTGGATT
 TCAGTTCCCTTTTGTGCCTTCATGCCTACTTCTTAATGCCTCTCTAAAGCCAAA

FIGURE 133

MEWWASSPLRLWLLFLFLPSAQGRQKESGSKWKVFDQINRSLNENYEPCCSSQNCSCYHGVIE
EDLTPFRGGISRKMMAEVVRRLGTHYQITKNRLYRENDCMFPSRCSGVEHFILEVIGRLPD
MEMVINVRDYPQVPKWMEPAIPVFSFSKTSEYHDIMYPAWTFWEGGPVWPIYPTGLGRWDL
FREDLVRSAQAQWPWKKKNSTAYFRGSRTSPERDPLILLSRKNPKLVD AEYTKNQAWKSMKDT
LGKPAAKDVHLVDHCKYKYLENFRGVAASFRFKHLFLCGSLVFHVGD EWLEFFYPQLKPWVH
YIPVKTDLSNVQELLQFVKANDDVAQEIAERGSQFIRNHLQMD DITCYWENLLSEYSKFLSY
NVTRRKGYDQIIPKMLKTEL



CACCCCTCCATTCTCGCC**ATG**GCCCTGCATGCTCCTGATCCCTGCTGCCCTCGCCTCTT
TCATCCTGGCCTTTGGCACCGGAGTGGAGTTCGTGCGCTTTACCTCCCTTCGGCCACTTCTT
GGAGGGATCCCGGAGTCTGGTGGTCCGGATGCCGCCAGGGATGGCTGGCTGCCCTGCAGGA
CCGCAGCATPCTTGGCCCCCTGGCATGGGATCTGGGGCTCCTGCTTCTATTPTGTTGGGCAGC
ACAGCCTCATGGCAGCTGAAAGAGTGAAGGCATGGACATCCCGGTACTTTGGGGTCCCTCAG
AGGTCACTGTATGTGGCTGCACTGCCCTGGCCTTGCAGCTGGTGATGCGGTACTGGGAGCC
CATACCCAAAGGCCCTGTGTTGTGGGAGGCTCGGGCTGAGCCATGGGCCACCTGGGTGCCGC
TCCTCTGCTTTGTGCTCCATGTCATCTCTGGCTCCTCATCTTTAGCATCCTTCTCGTCTTT
GACTATGCTGAGCTCATGGGCTCAAAACAGGTATACCTACCAGTGTGGGGCTGGGCAGTCC
TCTGGCCCTGAAGTCTCCCCGGGCTCTCAGACTTCTCCCACTGCGCCACCCAGTGATGTG
TGGAGCTGCTGACAGTGTGTGGGTGGTGCCATACCTGGGCACGGACCGTCTCCTCCTTGCT
TTCCTCCTTACCCTCTACCTGGGCTGGCTCACGGGCTTGATCAGCAAGACCTCCGCTACCT
CCGGGCCCAGCTACAAAGAAAACCTCCACGTCTCTCGGCCCCAGGATGGGGAGGCAGAG**T**
GAGGAGCTCACTCTGGTTACAAGCCCTGTTCTTCTCCTCTCCCACTGAATTCATAAATCCTTAAC
ATCCAGGCCCTGGCTGCTTCATGCCAGAGGCCCAAATCCATGGACTGAAGGAGATGCCCTT
CTACTACTTGAGACTTTATTCTCTGGGTCCAGCTCCATACCTAAATTCGAGTTTCAGCCA
CTGAACTCCAAGTCCACTTCTCACCAGCAAGGAAGAGTGGGGTATGGAAGTCATCTGTCCC
TTCACTGTTTAGAGCATGACACTCTCCCCCTCAACAGCCTCCTGAGAAGGAAAGGATCTGCC
CTGACCACTCCCCTGGCACTGTTACTTGCCTCTGCGCCTCAGGGGTCCCCTTCTGCAACGCT
GGCTTCCACTCCAAGAAGGTGGACCAGGGTCTGCAAGTTCAACGGTTCATAGCTGTCCCTCCA
GGGCCCAACCTTGCCTCACCACTCCCGGCCCTAGTCTCTGCACCTCCTTAGGCCCTGCCTCT
GGGCTCAGACCCCACTCATGAAGGGGATTCTCTGCTCTTAACCTCGATGACTTGGGGCTC
CCTGCTCTCCCGAGGAAGATGCTCTGCAGGAAAATAAAGTACGCCTTTTTCTAAAAA

FIGURE 135

MAPALLIIPALASFLAFTGTVEFVRFTSLRPLGGIPESGGFDARQGWLAALQDRSILAP
LAWDLGLLLLFVQGHSLMAAEVRKAWTSRYFGVLQRSILYVACTALALQLVMRYWEP1PKGFPV
LWEARAEWPATWVPLLCFVLHVISWLLIFSILLVFDYAEMLGKQVYYHVLGLGEPLAKSP
RALRLFSHLRHPVCEVLLTVLWVVPTLGTDRLLAFLTLTYLGLAHLSDQDQLRYLRAQLQR
KLHLLSRPDGCV

Signal sequence:

amino acids 1-13

Transmembrane domains:

amino acids 58-76, 99-113, 141-159, 203-222

N-myristoylation sites:

amino acids 37-43, 42-48, 229-235

FIGURE 136

CCGAGCACAGGAGATTGCCTGCGTTTAGGAGGTGGCTGCGTTGTGGGAAAAGCTATCAAGGA
 AGAAATTGCCAAACCATGTCTTTTTTCTGTTTTTCAGAGTAGTTCACAACAGATCTGAGTGT
 TTTAATTAAAGCATGGAATACAGAAAACACAAAAAAGCTTAAGCTTTAATTTTCATCTGGAATT
 CCACAGTTTTCTTAGCTCCCTGGACCCGGTTGACCTGTTGGCTCTTCCCGCTGGCTGCTCTA
 TCACGTGGTGCTCTCCGACTACTCACCCGAGTGTAAGAACCTTCGGCTCGCGTGCTTCTG
 AGCTGCTGTGGATGGCCCTCGGCTCTCTGGACTGTCTTCCGAGTAGGATGTCACTGAGATCC
 CTCAAATGGAGCCTCTGTGCTGTCACTCTGAGTTTTCTTTGTAGTGTGGTACCTCAGCCT
 TCCCCACTACAATGTGATAGAACGCGTGAACCTGGATGTACTTCTATGAGTATGAGCCGATTT
 ACAGACAAGACTTTCACCTTCACACTTCGAGAGCATTCAAAGTCTCTCATCAAAATCCATTT
 CTGGTCATTCTGGTGACCTCCACCCCTCAGATGTGAAAGCCAGGCAGGCCATTAGAGTTAC
 TTGGGGTGAAAAAAGTCTTGGTGGGGATATGAGGTCTTACATTTTTCTTATTAGGCCAAG
 AGGCTGAAAAGGAAGACAAAATGTGGCATTGTCTTAGAGGATGAACACCTTCTTTATGGT
 GACATAATCCGCACAAGATTTTTTAGACACATATAATAACCTGACCTTGAAAACCATTTATGGC
 ATTCAGGTGGGTAACCTGAGTTTTGCCCAATGCCAAGTACGTAATGAAGACAGACACTGATG
 TTTTCATCAATACTGGCAATTTAGTGAAGTATCTTTTAAACCTAAACCACTCAGAGAAGTTT
 TTCACAGGTTATCCTCTAATTGATAATTATTCCTATAGAGGATTTTACCAAAAACCCATAT
 TTCTTACCAGGAGTATCCTTCAAGGTGTTCCCTCCATACTGCAGTGGGTTGGGTTATATAA
 TGTCCAGAGATTTGGTGCCAAAGGATCTATGAAATGATGGGTGACGTAACCAACCATCAAGTTT
 GAAGATGTTTATGTCGGGATCTGTTGAATTTATTAAAGTGAACATTTCATATTCCAGAAGA
 CACAAATCTTTCTTTCTATATAGAATCCATTTGGATGTCTGTCAACTGAGACGTGTGATTG
 CAGCCCATGGCTTTTCTTCCAAGGAGATCATCACTTTTTGGCAGGTGATGCTAAGGAACACC
 ACATGCCATTATTAACTTCACATTCTACAAAAGCCTAGAAGGACAGGATACCTTGTGGAAA
 GTGTTAAATAAAGTAGGTACTGTGGAAAATTCATGGGGAGGTGAGTGTGCTGGCTTACACTG
 AACTGAAACTCATGAAAAACCCAGACTGGAGACTGGAGGGTTACACTGTGATTATTAGTCT
 AGGCCCTTCAAAGATGATATGTGGAGGAATTAATATATAAGGAATTGGAGTTTTTGTCTAAA
 GAAATTAATAGGACCAACAAATTTGGACATGTCATTCTGTAGACTAGAATTTCTTAAAAGGG
 TGTTACTGAGTTATAAGCTCACTAGGCTGTAAAAACAAACAATGTAGAGTTTTATTTATTG
 AACATGTAGTCACCTGAAGGTTTTGTGTATATCTTATGTGGATTACCAATTTAAAAATATA
 TGTAGTTCTGTGTCAAAAACCTTCTTCACTGAAGTTATACTGAACAAAATTTTACCTGTTTT
 TGGTCATTTATAAAGTACTTCAAGATGTTGCAGTATTTTACAGTTATTATTATTTAAAATTA
 CTTCAACTTTGTGTTTTTAAATGTTTTGACGATTTCAATACAAGATAAAAAGGATAGTGAAT
 CATCTTTTACATGCAACATTTTCCAGTTACTTAACTGATCAGTTTATTATTGATACATCAC
 TCCATTAAATGTAAAGTCATAGGTCATTATTGCATATCAGTAATCTCTTGACTTTGTTAAAT
 ATTTTACTGTGGTAAATATAGAGAAGAATTAAGCAAGAAAATCTGAAA

FIGURE 137

MASALWTVLPSRMSLRSLKWSLLLLSLLSFFVMWYLSLPHYNVIERVNWMYFYEYEPYRQD
FHFTLREHSNCSSHQNPFLVILVTSHPSDVKAQAIRVTWGEKKSWWGYEVLTFLLGQEA EK
EDKMLALSLEDEHLLYGDIIRQDFLDTYNNLT LKTIMAFRWVTEFCPNAKYVMKTD TDVFIN
TGNLVKYLLNLNHSEKFFTGYPLIDNYSYRGFYQKTHISYQEYPFKVFPYPYCSGLGYIMSRD
LVPRIYEMMGHV KPIKFEDVYVGICLNLLKVNIHIPEDTNLFFLYRIHLDVCQLRRVIAAHG
FSSKEIITFWQVMLRNTTCHY

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FIGURE 138

CCTCTGTCCACTGCTTTTCGTGAAGACAAGATGAAGTTCACAATTGTCTTTGCTGGACTTCTT
GGAGTCTTTCTAGCTCCTGCCCTAGCTAACTATAATATCAACGTCAATGATGACACAACAA
TGCTGGAAGTGGGCAGCAGTCAGTGAGTGTCAACAATGAACACAATGTGGCCAATGTTGACA
ATAACAACGGATGGGACTCCTGGAATTCATCTGGGATTATGGAAATGGCTTTGCTGCAACC
AGACTCTTTCAAAAGAAGACATGCATTGTGCACAAAATGAACAAGGAAGTCATGCCCTCCAT
TCAATCCCTTGATGCACTGGTCAAGGAAAAGAAGCTTCAGGGTAAGGGACCAGGAGGACCAC
CTCCAAGGGCCTGATGTACTCAGTCAACCCAAACAAAGTCGATGACCTGAGCAAGTTCGGA
AAAAACATTGCAAACATGTGTCTGGGATTCCAACATACATGGCTGAGGAGATGCAAGAGGC
AAGCCTGTTTTTTTACTCAGGAACGTGCTACACGACCAGTGTACTATGGATTGTGGACATTT
CCTTCTGTGGAGACACGGTGGAGAACTAAACAATTTTTTAAAGCCACTATGGATTTAGTCAT
CTGAATATGCTGTGCAGAAAAAATATGGGCTCCAGTGGTTTTTACCATGTCATTCTGAATT
TTTCTCTACTAGTTATGTTTGATTTCITTAAGTTTCAATAAAATCATTTAGCATTGAAAAAA

FIGURE 139

MKFTIVFAGLLGVFLAPALANYNINVNDNNNAGSQQSVSVNNEHNVANVDNNNGWDSWNS
IWDYGNQFAATRLFQKKTICIVHKMNKEVMPSIQSLDALVKEKKLQGKGPGGPPPKGLMYSVN
PNKVDDLKSKFGKNIANMCRGIPTYMAEEMQEASLFFYSGTCYTTSVLWIVDISFCGDTVEN

Signal Peptide:

amino acids 1-20

N-myristoylation Sites:

amino acids 67-72, 118-123, 163-168

Flavodoxin protein homology:

amino acids 156-174

CAATTTCTGAAACTAATCGTGTGACGAATTGACTTTGAAGCATTGCTTTTACAGAAGTATA
TTAACTTTTTAGGAGTAATTTCTAGTTGGATTGTAATATGAAATAATTTAAAGGGCTTCG
CTCATATATAGGAAAATCGCATATGGTCCTAGTATTAAATCTTATTGCTTACTGATTTTTT
TGAGTTAAGAGTTGTTATATGCTAGAATATGAGGATGTGAATATAAATAAGAGAAGAAAAA
GAATTAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAACTGGTTGTGTACATG
CAAGCTTATAGTTGAAATATTTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGT
TTGTTTCGATTTC AACCGAGACTATAGCATGTGCTTGCATCTACCTTGCAGCTAGAGCACTT
CAGATTCGGTTGCCAACTCGTCCCCATTGGTTTCTTCTTTTTGGTACTACAGAAGAGGAAAT
CCAGGAAATCTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTAC
TGGAAAAAGAAGTAGAAAAAGAAAAGTAGCCCTTACAAGAAGCCAAATTAAGCAAAGGGA
TTGAATCCGGATGGAACCTCAGCCCTTTCAACCTTGGGTGGATTTTCTCCAGCTCCAAGCC
ATCATCACCAAGAGAGTAAGAGCTGAAGAGAAATCCAATCTCCATTATGTGTGAAGAC
TCAAAAAAGCAACCTGAGATAGAGACAACAGGCTTCCAAAAGCCCTTACAAGTGGTGTAGAAAA
GACAGCAAGAGAAGTAGAATAGCAGAAGTGCAAGTCGATCGAGGTCAAGAACACGATCACG
TTCTAGATCACATACTCCAAGAAGACACTATAATAATAGGCGGAGTCGATCTGGAACATACA
GCTCGAGATCAAGAAGCAGGTCCCGCAGTCACAGTGAAAGCCCTCGAAGACATCATAATCAT
GGTTCCTCTCACCTTAAGGCCAAGCATACCAGAGATGATTTAAAAAGTTCAAACAGACATGG
TCATAAAAGGAAAAAATCTGTTCTCGATCTCAGAGCAAGTCTCGGGATCACTCAGATGCAG
CCAAGAAACACAGGCATGAAAGGGGACATCATAGGGACAGGCGTGAACGATCTCGCTCCTTT
GAGAGGTCCCATAAAGCAAGCACCATGGTGGCAGTCGCTCAGGACATGGCAGGCACAGGCG
CTGA

CTTGTCTTCTCTCTTTGAGCCTGCATCAGTTCTTGGTTTTGCCTATCTACAGTGTGATGT
ATGGACTCAATCAAAAACATTAAACGCAAACCTGATTAGGATTGATTTCTTGAAACCCCTCTA
GGTCTCTAGAACACTGAGGACAGTTTCTTTTGAAAGAAGTATGTTAATTTTTTTGCACATT
AAAATGCCCTAGCAGTATCTAATTAAAAACCATGGTCAGGTTCAATTGTACTTTATTATAGT
TGTGTATTGTTTATTGCTATAAGAACTGGAGCGTGAATCTGTAAAAATGTATCTTATTTTT
ATACAGATAAAATTCAGACACTGTTCTATTTAAGTGGTTATTTGTTTAAATGATGGTGAAT
ACTTTCTTAACACTGGTTGTCTGCATGTGTAAAGATTTTACAAGGAAATAAAATACAAAT
CTTGTTTTTCTAAAAAAGAAAAAAGT

FIGURE 141

MNDSLRTNVFVRFPETIACACIYLAARALQIPLPTRPHWFLLFGTTTEEEIQEICIETLRLY
 TRKKPNYELLEKEVEKRKVALQEAKLKAKGLNPDGTPALSTLGGFSPASKPSSPREVKAEK
 SPISINVKTVKKEPEDRQQASKSPYNGVRKDSKRSRNSRSASRSRSTRSRSRSHTPRRHYN
 NRRSRSGTYSSRSRSTRSHSESPRRHHNHGSPHLKAKHTRDDLKSSNRHGHKRRKRSRSQ
 SKSRDHSDAAKKHRHERGHHRDRERSRSFERSHKSKHHGGSRSRGHGRHR

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FIGURE 142

TGGGGATAAAGGAAAAATGGTCAGGTATTAATGGCTTAAAGATTATTGGAAGGGGTTTATCA
TTTTTTGAANNATTTCGGGTCANAATTGNCTTTGAAAAGCATTGCTTTTTACAGAAATATAT
TANCTTTTATAGTAATTTCTAGTTTGGATTGTAATATGAAATTATTTAAAAGGGCTTCGCT
CATATATAGGAAAATCGCATATGGTCCTAGTATTAAATTNTTATTGCTTACTGATTTTTTTG
AGTTAAGAGTTGTTATATGNTAGAAATATGAGGATGTGAATATAAATAAGAGAAGAAAAAGA
ATAAAGTAGATTGAGTCTCCAATTTTATGTAAGCTTCAGAAGAAGCTGGTTTGTTCATGCA
AGCTTATAGTTGAAATATTTTTCAGGAATTACATGAATGACAGTCTTCGAACCAATGTGTTT
GTTCGATTTCAACCAGAGANTATAGCATGTGCTTGCATCTACCTTGCAGNTAGAGCACTTCA
GATTCGGTTGCCAACTNGTCCCATTTGGTTTCTTCTTTTTGGTACTACAGAAGAGGAAATCC
AGGAAATNTGCATAGAAACACTTAGGCTTTATACCAGAAAAAGCCAACTATGAATTACTG
GAAAAAGAAGTAGAAAAAAGAAAAGTAGCCTTACAAGAAGCCNAATTTAAAGCAAAGGGATT
GAATCCGGATGGAACCTCCAGCCCTTTCACCCCTGGGTGGATTTTCTCC

FIGURE 143

GGACACGAGGCCTCGTGCCAAGCTTGGCACGAGGGTGCACCGCGTTCTCGCACGCGT**ATGGC**
 GGTCTCTCGGAGTACAGCTGGTGGTGACCTGCTCACTGCCACCTCATGACAGGCTGGCGC
 CACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAAACGGCAGTTTGTTCGATACAAGCACCCG
 TCTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCCAGAGGCAGGAAAGAGCGGTG
 GGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCGAGATGCCCCGTTCAGCTGG
 AGACCTGCCCCCTCACGACCTGGATGCCCTGGTCTGCGCTTCTTCTGGAGTACCAGTGG
 TTTGTGGACTTTGCTGTGTACTCGGGCGGCGTGTACCTCTTCACAGAGGCCTACTACTACAT
 GCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGTGCCTGCTCACGGTGACCTTCT
 CCATCAAGATGTTCTCTGACAGTGACACGGCTGTACTTCAGCGCCGAGGAGGGGGTGAGCGC
 TCTGTCTGCCTCACCTTTGCCTTCTCTCTCCCTGCTGCTGGCCATGCTGGTGAAGTGGTGGC
 GGAGGAGACCCCTCGAGCTGGGCCCTGGAGCCTGGTCTGGCCAGCATGACCCAGAACCTAGAGC
 CACTTCTGAAGAAGCAGGGCTGGGACTGGGCGCTTCTGTGGCCAAGCTGGCTATCCGCGTG
 GGACTGGCAGTGGTGGGCTCTGTGCTGGGTGCCTTCTCACCTTCCCAGGCCCTGCGGCTGGC
 CCAGACCCACCGGGACGCACTGACCATGTGCGAGGACAGACCCATGCTGCAGTTCTCTCTGC
 ACACCAGCTTCTGTCTCCCTGTTATCCTGTGGCTCTGGACAAAGCCCATTGCACGGGAC
 TTCCTGCACACGCCCGCTTTGGGGAGACGCGTTTCTCCCTGCTGTCCGATTCTGCCTTCGA
 CTCTGGGGCGCTCTGGTTGCTGGTGGTGTGCTGCTGCGGCTGGCGGTGACCCGGCCCCC
 ACCTGCAGGCCTACCTGTGCCTGGCCAAGGCCCGGGTGGAGCAGCTGCGAAGGGAGGCTGGC
 CGCATCGAAGCCCGTGAAATCCAGCAGAGGGTGGTCCGAGTCTACTGCTATGTGACCGTGGT
 GAGCTTGCAGTACCTGACGCGCTCATCCTCACCCTCAACTGCACACTTCTGCTCAAGACGC
 TGGGAGGCTATTCTGGGGCTGGGCCAGCTCCTCTACTATCCCCGACCCATCTCAGCC
 AGCGCTGCCCCCATCGGCTCTGGGGAGGACGAAGTCCAGCAGACTGCAGCGCGGATTGCCGG
 GGCCCTGGGTGGCTGCTTACTCCCTCTTCTCCGTGGCGTCTGGCCTACCTCATCTGGT
 GGACGGCTGCCTGCCAGCTGCTGCCAGCCTTTTCGGCCTCTACTTCCACCAGCACTTGGCA
 GGCTCC**TAG**CTGCCTGCAGACCCCTCCTGGGGCCCTGAGGTCTGTCTCTGGGGCAGCGGGACA
 CTAGCCTGCCCCCTCTGTTTGCGCCCCCGTGTCGCCAGCTGCAAGGTGGGGCCGGACTCCCC
 GCGTTCCCTTACCACAGTGCCTGACCCGCGGCCCCCCCTTGGACGCCGAGTTTCTGCCTCA
 GAACTGTCTCTCTGGGCCAGCAGCATGAGGGTCCCGAGGCCATTGTCTCCGAAGCGTATG
 TGCCAGGTTTGTAGTGGCGAGGGTGATGCTGGTGTCTTCTGAACAAATAAAGGAGCATGCC
 GATTTTAA

FIGURE 144

MAVLGVQLVVTLLTATLMHRLAPHCSFARWLLCNGSLFRYKHPSEELRALAGKPRPRGRKE
RWANGLSEEKPLSVPRDAPFQLETCPLTTVDALVLRFFLEYQWFVDFAVYSGGVYLFTEAYY
YMLGPAKETNIAVFWCLLTVTFSIKMFLT VTRLYFSAEEGGERSVCLTF AFLFLLLAMLVQV
VREETLELGLPGLASMTQNLEPLLKKQGWDPVAKLAIRVGLAVVGSVLGAFTFPGLR
LAQTHRDALTMSEDRPMLQFLLHTSFLSPLFILWLWTKPIARDFLHQPPFGETRFSLLSDSA
FDSGRLWLLVVLCLLRLAVTRPHLQAYLCLAKARVEQLRREAGRIEAREIQQRVVRVYCYVT
VVS LQYLTPLILTLNCTLLKTLGGYSWGLGPAPLLSPDPSSASAAPIGSGEDEVQQTAARI
AGALGGLLTPLFLRGVLAYLIWWTAACQLLASLFGLYFHQHLAGS

FIGURE 145

CGTTNGCACGCGTCAATGGCGGTCTCGGAGTACAGCTGGTGGTGACCCCTGCTCACTGCCAC
 CCTCATGCACAGGCTGGCGCCACACTGCTCCTTCGCGCGCTGGCTGCTCTGTAACGGCAGTT
 TGTTCCGATACAAGCACCCGTNTTGAGGAGGAGCTTCGGGCCCTGGCGGGGAAGCCGAGGCC
 CAGAGGCAGGAAAGAGCGGTGGGCCAATGGCCTTAGTGAGGAGAAGCCACTGTCTGTGCCCC
 GAGATGCCCCGTTCCAGCTGGAGACCTGCCCCCTCACGACCGTGGATGCCCTGGTCCTGCGC
 TTCTTCCTGGAGTACCAGTGGTTTGTGGACTTTGCTGTGTACTCGGCGGGCGTGTACCTCTT
 CACAGAGGCCTACTACTACATGCTGGGACCAGCCAAGGAGACTAACATTGCTGTGTTCTGGT
 GCCTGCTCACAGTGACCTTCTCCATCAAGATGTTCTTGACAGTGACACGGCTGTACTTCAGC
 GCCGAGGAGGGGGGTGAGCGCTCTGTCTGCCTCACCTTTGCCTTCCTCTTCCTGCTGCTGGC
 CATGCTGGTGCAAGCG

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FIGURE 146

GGTTCCTACATCCTCTCATCTGAGAATCAGAGAGCATAATCTTCTTACGGGGCCCGTGATTATTAAAGTGGCTT
 AATCTGAAGGTTCTCAGTCAAATCTTTGTGATCTACTGATTGTGGGGGCATGCGAAGGTTTGCTTAAAGGAGC
 TTGGCTGGTTTGGGCGCTTGTAGCTGACAGAAGGTGGCCAGGAGAATGACGACACTGCTCGGAGAATGAAGG
 CGCTTCTGTGCTGGTCTTGCCTTGGCTCAGTCTCTGTAACATACATTGACAAATGTGGGCAACCTGCATCTCCTG
 TATTGAGAATCTGTAAAGTGCCTCCACTACGGCCTGACCAAAGATAGGAAGAGGCGCTCACAGATGGCTG
 TCCAGACGGCTGTGCGAGCCTCACAGCCAGCGCTCCCTCCCCAGAGGTTTCTGCAGCTGCCACCATCTCCTTAA
 TGACAGACGAGCCTGGCTAGACACCTGCTACGTCTCCTCGGAGAGGACGGGACGCCAGCAATCAGCCCA
 GTGGACTCTGGCCGGAGCAACCGAATAGGGCACGGCCCTTGAGAGATCCACTATTAGAAGCAGATCATTTAA
 AAAATAAATCGAGCTTTGAGTGTCTTGAAGGACAAAGACGGGAGTGCAGTTGCCAACCATGCCGACGAGG
 GCAGGGAAAATTCTGAAAACCCACTGCCCTGAAGTCTTTCCAAGGTTGTACCACCTGATTCAGATGGTGAA
 ATTACAGCATCAAGATCAATCGAGTAGATCCAGTGAAAGCCTCTCTATTAGGCTGGTGGGAGGTAGCGAAAC
 CCCACTGGTCCATATCATTTATCAACACATTTATCGTGATGGGGTGATCGCCAGAGACGGCCCGCTACTGCCAG
 GAGACATCATTTAAAGTCAACGGGATGGACATCAGCAATGTCCCTCACAACTACGCTGTGCGTCTCCTCGCG
 CAGCCCTGCCAGGTGCTGTGGCTGACTGTGATGCGTGAACAGAAGTCCGACAGGAAACATGGACAGGCCCC
 GGATGCTACAGACCCCGAGATGACAGCTTTCATGTGATTCTCAACAAAAGTAGCCCCGAGGAGCAGCTTGGAA
 TAAACTGGTGCGCAAGGTGGATGAGCCTGGGGTTTTTCATCTTCAATGTGCTGGATGGCGGTGTGGCATATCGA
 CATGGTCAGCTTGAGGAGAATGACCGTGTGTAGCCATCAATGGACATGATCTTCGATATGGACGCCAGAAAG
 TCGCGCTCATCTGATTAGGCCAGTGAAGACGTGTTCACTCGTGTGCCCGAGGTTCCGCAGCGGAGGCC
 CTGACATCTTTCAGGAAGCCGGCTGGAACAGCAATGGCAGCTGGTCCCCAGGGCCAGGGGAGAGGAGCAACACT
 CCCAAGCCCCCTCATCTCAATTAATTTGTCTATGAGAAGGTGTAATATCCAAAAAGACCCCGGTGAATCTCT
 CGGCATGACCGTCGACGGGGGAGCATCACATAGAGAATGGGATTTGCCTATCTATGTCACTAGTGTGAGCCCG
 GAGGAGTCATAAGCAGAGATGGAAGAATAAAAAACAGGTGACATTTTGTGAATGTGGATGGGGTCGAATGACA
 GAGGTGAGCCGAGTGAAGCAGTGGCATTTATGAAAAGAACATCATCTCGATAGTACTCAAAGCTTTGGAAGT
 CAAAGATGATGAGCCCCAGGAGACTGCAGCAGCCAGCAGCCCTGACTCCAACCACAACATGGCCCCACCCA
 GTGACTGTGCTCCCATCTGGGTCTGTGGCTGGAATTACACAGGTGCTTGTATAACTGTAAGATATTGTATTA
 CGAAGAAACACAGCTGGAAGTCTGGGCTTCTGCATTGAGGAGGTATGAAGATACATGGAAACAAACCTTT
 TTTTCATCAAATCCATTGTTGAAGGAACACAGCATACATGATGGAAGAATTAGATGTGGTGATATTCTCTTG
 CTGTCAATGGTAGAAGTACATCAGGAATGATACATGCTTGCTTGGCAAGACTGCTGAAAGAACTTAAAGGAAGA
 ATTACTCTAACTATTGTTCTTGGCCTGGCACTTTTTTATGAATCAATGATGGGTGAGGAAACAGAAAAA
 TCACAAATAGGCTAAGAAGTTGAACACATATATTTATCTGTCACTTTTATATTTAAAGAAAGAAATCAATTGT
 AAAAATGTCAGGAAAGATGATCATCTAATGAAAGCAGTTACACCTCAGAAAAATGATTTCCAAAAAATTA
 AAATCTAGTTTTTTTTTTCAGTGTGGAGATTCTCATTACTACAACTATGTTTATATTTTTTCTATTCAAT
 AAAAGCCCTAAAAACAATAAAATGATTGATTGTATACCCACTGAATCAAGCTGATTTAAATTTAAATTT
 GGTATATGCTGAAGTGCAGAGGTACATTTATGCCATTTTTTAATTTACAGCTAAATATTTTTTAAATGCA
 TTGCTGAGAAACGTTGCTTTCATCAACAAGATAAATATTTTTTCAGAGTTAAA

FIGURE 147

MKALLLLVLPWLS PANYIDNVGNLHFLYSELCKGASHYGLTKDRKRRSQDGC PDGCASLTAT
APSPEVSA AATISLMTDEPGLDNPAYVSSAEDGQPAISPVD SGRSNRTRARPFERSTIRSR S
FKKINRALSVLRRTKSGSAVANHADQGRENSENTTAEVVFRLYHLI PDGEITSIKINRVDP
SESLSIRLVGGSETPLVHIIIQHIIYRDGVIARDGRLLPGDIILKVNGMDISNVPHNYAVRL L
RQPCQVLWLTVMREQKFRSRNNGQAPDAYRPRDDSFHVILNKSSPEEQLGIKLV RKVDEPGV
FIFNVLDGGVAYRHGQLEENDRVLAINGHD LRYGSPESA AHLIQASERRVHLVVS RQVRQRS
PDFQEAGWNSNGSWSPGPGERSNTPKPLHPTITCHEKV VNIQKDPGESLGMTVAGGASHRE
WDLPIYVISVEPGGVISRDGRIKTDILLNVDGVELTEVSRSEAVALLKRTSSSIVLKALEV
KEYEPQEDCSSPAALDSNHNMAPPSDWSF SWVMWLELPRCLYNCKDIVLRRNTAGSLGFCIV
GGYEEYNGNKPF FIKSIVEGTPAYNDGRIRCGDILLAVNGRSTSGMIHACLARLLKELKGRI
TLTIVSWPGTFL

FIGURE 148

CCAAAGTGATCATTTGAAAAAGAGATATCCACATCTTCAAGCCCATATAAAGGATAGAAGCT
GCACAGGGCAGCTTTACTTTACTCCAGCACCTTCCTCTCCAGGCAAAATGGTGCTGACCATCT
TTGGGATACAATCTCATGGATACGAGGTTTTTAACATCATCAGCCCAAGCAACAATGGTGGC
AATGTTCAGGAGACAGTGACAATTGATAATGAAAAAATACCGCCATCGTTAACATCCATGC
AGGATCATGCTCTTCTACCACAATTTTTGACTATAAACATGGCTACATTGCATCCAGGGTGC
TCTCCCGAAGAGCCTGCTTTATCCTGAAGATGGACCATCAGAACATCCCTCCTCTGAACAAT
CTCCAATGGTACATCTATGAGAAACAGGCTCTGGACAACATGTTCTCCAACAAATACACCTG
GGTCAAGTACAACCCCTCTGGAGTCTCTGATCAAAGACGTGGATTGGTTCTGCTTGGGTCAC
CCATTGAGAACTCTGCAAACATATCCCTTTGTATAAGGGGGAAGTGGTTGAAAACACACAT
AATGTCGGTGCTGGAGGCTGTGCAAAGGCTGGGCTCCTGGGCATCTTGGGAATTTCAATCTG
TGCAGACATTCTGTTTAGGATGATTAGCCCTCTTGTTTTATCTTTTCAAAGAAATACATCC
TTGGTTTACACTCAAAGTCAAATTAATTCTTTCCCAATGCCCAACTAATTTTGAGATTC
AGTCAGAAAATATAAATGCTGTATTTATA

FIGURE 149

MKILVAFVLVLTIFGIQSHGYEVFNIISPSNNGGNVQETVTIDNEKNTAIVNIHAGSCSSTT
IFDYKHGYIASRVLSRRACFILKMDHQNIPLNQLQWYIYEKQALDNMFSNKYTWVKYNPLE
SLIKDVDWFLLGSPIEKLCKHIPLYKGEVVENTHNVGAGGCAKAGLLGILGISICADIHV

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FIGURE 150

GGCACGAGCCAGGAAC TAGGAGGTTCTCACTGCCCGAGCAGAGGCCCTACACCCACCGAGGC
ATGGGGCTCCCTGGGCTGTTCTGCTTGCCCGTGCTGGCTGCCAGCAGCTTCTCCAAGGCACG
 GGAGGAAGAAATTACCCCTGTGGTCTCCATTGCCTACAAAGTCC TGGAAGTTTCCCCAAAG
 GCCGCTGGGTGCTCATAACCTGCTGTGCACCCAGCCACACCGCCCATCACCTATTCCCTC
 TGTGGAACCAAGAACATCAAGGTGGCCAAGAAGTGGTGAAGACCCACGAGCCGGCCTCCTT
 CAACCTCAACGTCACTCAAGTCCAGTCCAGACCTGCTCACCTACTTCTGCCGGGCGTCCT
 CCACCTCAGGTGCCCATGTGGACAGTGCCAGGCTACAGATGCACTGGGAGCTGTGGTCCAAG
 CCAGTGTCTGAGCTGCGGGCCAACTTCACTCTGCAGGACAGAGGGGCAGGCCCCAGGGTGGA
 GATGATCTGCCAGGCGTCCTCGGGCAGCCCACCTATACCAACAGCCTGATCGGGAAGGATG
 GGCAGGTCCACCTGCAGCAGAGACCATGCCACAGGCAGCCTGCCAACTTCTCCTTCTGCGG
 AGCCAGACATCGGACTGGTTCTGGTGCCAGGCTGCAAAACACGCCAATGTCCAGCACAGCGC
 CCTCAGTGGTGCCCCAGGTGGTGACCAGAAGATGGAGGACTGGCAGGGTCCCCTGGAGA
 GCCCCATCCTTGCCCTTGCCGCTCTACAGGAGCACCCGCCGCTCTGAGTGAAGAGGAGTTTGGG
 GGGTTCAGGATAGGGAATGGGGAGGTGAGGAGACGCAAGCAGCAGCCATG TAGAATGAACC
 GTCCAGAGAGCCAAGCACGGCAGAGGACTGCAGGCCATCAGCGTGCACTGTTTCGTATTGGGA
 GTTCATGCAAAATGAGTGTGTTTTAGCTGCTCTGCCACAAAAAAAAAAAAAAAAAAAAAA

FIGURE 151

MGLPGLFCLAVLAASSFSKAREEEITPVVSIAYKVLVFPKGRWVLITCCAPQPPPPITYSL
CGTKNIKVAKKVVKTHEPASFNLVTLKSSPDLLTYFCRASSTSGAHVDSARLQMHWELWSK
PVSELRANFTLQDRGAGPRVEMICQASSGSPITNSLIGKDQVHLQQRPCRQPANFSFLP
SQTSDWFWCQAANNANVQHSALTVPVPGGDQKMEDWQGPLESPILALPLYRSTRRLSEEEFG
GFRIGNGEVRGRKAAAM

Signal Peptide:

amino acids 1-18

N-glycosylation Sites:

amino acids 86-89, 132-135, 181-184

FIGURE 152

GGTCCTTAATGCGCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTG
 CTGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCCCTACTCTCTTTGCTATGACATCACCGT
 CATCCCTAAGTTTACAGCTTGACCCAGGTGGTGTGCGGTTCAAGGCCAGTGGATGAAAAGA
 CTTTTCTTCACTATGACTGTGGCAACAAGACAGTACACCTGTCACTCCCTGGGGAAGAAA
 CTAAATGTCAACCGCCTGGAAAGCACAGAACCAGTACTGAGAGAGGTGGTGGACATACT
 TACAGAGCAACTGCGTGACATTGAGCTGGAGAATTACACACCCAAAGGAACCCCTCACCTGCG
 AGGCAAGGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGT
 TTCGATGGGCAGATCTTCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCC
 TGGAGCCAGAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCTTCCATT
 ACTTCTCAATGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACC
 CTGGAGCCAAGTGCAGGAGCACCCTCGCCATGTCTCAGGCACAACCCAACCTCAGGGCCAC
 AGCCACCACCCTCATCCTTTGCTGCCTCCTCATCCTCCCTGCTTCATCCTCCCTGGCA
 TCTGAGGAGAGTCTTTAGAGTGACAGGTTAAAGCTGATACCAAAAGGCTCCTGTGAGCAG
 GTCTTGATCAAATCGCCCTTCTGTCTGGCCAGCTGCCACGACCTACGGTGTATGTCCAGT
 GGCTCCAGCAGATCATGATGACATCATGGACCCAATAGCTCATTCACTGCCTTGATTCCTT
 TTGCCAACAATTTTACCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACC
 TGATGGAATTCCTGCACCTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTCTCTC
 TCTTTTGTGTTGGAAAATCAAGTACTTCTTTGAATGATGATCTCTTTCTTGCAAAATGATATT
 GTCAGTAAATAATCACGTTAGACTTCAGACCTCTGGGGATTCTTTCCGTGTCCTGAAAGAG
 AATTTTAAATTTTAAATAAGAAAAAATTTATATTAATGATTGTTTCTTTAGTAATTTAT
 TGTCTGTACTGATATTTAAATAAAGAGTTCTATTCCCAAAAAAAAAAAAAAAAAA

FIGURE 153

MAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRGPRWCVAQGVQDEKFTL
HYDCGNKTVTPVSPLGKKNVTTAWKAQNPNVLEVVLDILTEQLRDIQLENYTPKEPLTLQAR
MSCEQKAEGHSSGSWQSFDFGQIFLLFDSEKRMWTVHPGARKMKEKWENDKVVAMSFHYFS
MGDCIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

Important features:

Signal peptide:

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

FIGURE 154

GGGAAAGCCATTTGAAAACCCATCTATACAACTATATATTTTCATTTCTGCTGCTAGCTG
CCTTGGGCCTCACAATTTTCATTCTGTTTTCTGACTTTCAAGTTATATACCGTGGAAATGGAG
TTGATCCCAACCATAACATCGTGGAGGGTTTTAATTTTGGTGGTAGCCCTCACCCAATTCTG
GTGTGGCTTTCCTTGCAGAGGATTCCACCTTCAAAATCATGAACTCTGGCTGTTGATCAAAA
GAGAATTTGGATTCTACTCTAAAAGTCAATATAGGACTTGGCAAAAAGAAGCTAGCAGAAGAC
TCAACCTGGCCTCCCATAAACAGGACAGATTATTCAGGTGATGGCAAAAATGGATTCTACAT
CAACGGAGGCTATGAAAGCCATGAACAGATTCCAAAAAGAAAATCAAATTGGGAGGCCAAC
CCACAGAACAGCATTTCTGGGCCAGGCTGTAATCAGAATTGTCGTCGTACATGCTCAACAGC
ATTGCTTTTTTCCCCAAAATTAACACATTGTGGAGAAGTGATGATACTCTCCCCTTACCTTT
CCTCTCTCCATTCAAGCATTCAAAGTATATTTTCAATGAATTAACCTTGCAGCAAGGGACC
TTAGATAGGCTTATTCTGACTGTATGCTTTACCAATGAGAGAAAAAATGCATTTCCTGTAT
CATCCTTTTCAATAAACTGTATTCAATTTGAAAAAAAAAAAAAAAAAAAAA

FIGURE 155

MELIPTITSWRVLILVVALTQFWCGFLCRGFHLQNHFWLLIKREFGFYSKSQYRTWQKKLA
EDSTWPPINRTDYSGDGKNGFYINGGYESHEQIPKRKLKLGQPTEQHFWARL

FIGURE 156

GTTCTCCTTTCCGAGCCAAAATCCCAGGCGATGGTGAATTATGAACGTGCCACACC**ATGAAG**
 CTCTTGTGGCAGGTAAGTGTGCACACCACACCTGGAATGCCATCCTGCTCCCGTTCGTCTA
 CCTACGGCGCAAGTGTGGATTCTGTGTGCAGCCATCGCTGCTGCCGGCTCAGCCGGGCCCC
 AGAAGTGCCTCCGTTTGTCTGTGCAGTAACAGTTTCAGCAAGGTGGTGTGCACGCGCCGG
 GGCCTCTCCGAGGTCCCAGGCGTATTCCCTCGAACACCCGGTACCTCAACCTCATGGAGAA
 CAACATCCAGATGATCCAGGCGGACACCTTCCGCCACCTCCACCACCTGGAGGTCTCGAGT
 TGGGCAGGAAGTCCATCCGGCAGATTGAGGTGGGGGCTTCAACGGCCTGGCCAGCCTCAAC
 ACCCTGGAGCTGTTTCGACAACTGGCTGACAGTTCATCCCTAGCGGGGCTTTGAATACCTGTC
 CAAGCTGCGGGAGCTCTGGCTTCGCAACAACCCATCGAAAGCATCCCTCTTACGCTTCA
 ACCGGTGCCCTCCCTCATGCGCTGGACTTGGGGGAGCTCAAGAAGCTGGAGTATATCTCT
 GAGGGAGCTTTTGGGGGCTGTTCAACCTCAAGTATCTGAAGTTGGGCATGTGCAACATTAA
 AGACATGCCCAATCTCACCCCTGGTGGGGCTGGAGAGCTGGAGATGTGAGGGAACCACT
 TCCCTGAGATCAGGCTGGCTCCTTCCATGGCTGAGCTCCCTCAAGAAGCTCTGGGTCTATG
 AACTCACAGGTGAGCTGATTGAGCGGAATGCTTTGACGGGCTGGCTTCACTTGTGGAAGT
 CAAGTTGGCCCAATAAAGCTCTCTTCTTTGCCCATGACCTCTTTACCCCGCTGAGGTACC
 TGGTGGAGTTGCATCTACACCACAACCTTGGAACTGTGATTGTGACATCTGTGGCTAGCC
 TGGTGGCTTCGAGAGTATATACCCACCAATTCCACCTGCTGTGGCGGTGTATGCTCCCAT
 GCACATGCGAGCGCTACCTCGTGGAGGTGGACAGGCTCCTTCCAGTGCTCTGCCCTCTG
 TCATCATGGACGCACCTCGAGACCTCAACATTCTGAGGGTGGATGGCAGAACTTAAGTGT
 CGGACTCCCCCTATGTCTCCGTGAAGTGGTTGCTGCCCAATGGGACAGTGCTCAGCCACGC
 CTCCCGCCACCAAGGATCTCTGTCTCAACGACGGCACCTTGAAGTTTCCACGCTGTGTC
 TTTAGACACTGGGGTGTACACATGCATGGTGACCAATGTTGCAGGCAACTCCAACGCCTCG
 GCCTACCTCAATGTGAGCACGGCTGAGCTTAACACCTCCAACATACAGCTTCTTCAACACAGT
 AACAGTGGAGACCACGGAGATCTCGCTGAGGACACAACGCGAAAGTACAAGCCTGTTCCCTA
 CCAGTCCACTGGTTACAGCGGCATATACCACCTCTACACCGGTGCTCATTAGAGTACC
 CGTGTGCCCAAGCAGGTGGCAGTACCCGCGACAGACACCACTGACAAGATGCAGACCAGCT
 GGATGAAGTCATGAAGACCACCAAGATCATCATTTGGCTGCTTTGTGGCAGTGACTCTGCTAG
 CTGCCGCATGTTGATTGTCTTCTATAAACTTCGTAAGCGGCACAGCAGCGGAGTACAGTC
 ACAGCGCGCCGGACTGTTGAGATAATCCAGGTGGACGAAGACATCCCAGCAGCAACATCCGC
 AGCAGCAACAGCAGCTCCGTCGGTGTATCAGGTGAGGGGGCAGTAGTGCTGCCCAATTC
 ATGACCATATTAACTACAAACACCTACAACACGACAGTGGGGCCACTGGACAGAAAACAGC
 CTGGGGAAGTCTCTGCACCCACAGTCAACCATCTCTGAACCTTATATAATTACAGACCA
 TACCAAGGACAAGGTACAGGAAGTCAAATA**TGA**CTCCCTCCCCAAAAAAGCTTATAAAT
 GCAATAGAATGCACACAAAGACAGCAACTTTTGTACAGAGTGGGGAGAGACTTTTCTTGTGA
 TATGCTTATATATTAAGTCTATGGCTGGTTAAAAAAAACAGATTATATTAATAATTTAAAGA
 CAAAAAGTCAAAACA

FIGURE 157

MKLLWQVTVHHHTWNAILLPFVYLTAQVWILCAAIAAASAGPQNCPSVSCSNQFSKVVCT
RRGLSEVPQGIPSNTRYLNLMENNIQMIQADTFRHLHHLEVLQLGRNSIRQIEVGAFNGLAS
LNTLELFDNWLTVIPSGAFEYLSKLRELWLRNNPIESIPSYAFNRVPSLMRLDLGELKKLEY
ISEGAFEGFLFNLYLNLGMCNIKDMPNLTPLVGLLEELEMSGNHFEIRPGSFHGLSSLKKLW
VMNSQVSLIERNADFGLASLVELNLAHNNLSSLPHDLFTPLRYLVELHLHHNPWNCDILW
LAWWLREYIPTNSTCCGRCHAPMHMRGRYLVEVDQASFQCSAPFIMDAPRDLNISEGRMAEL
KCRTPPMSSVKWLLPNGTVLSHASRHPRISVLNDGTLNFSHVLLSDTGVYTCMVTNVAGNSN
ASAYLNVSTAE LN TSNYSFFT VTVETTEISPEDTTRKYKPVPTTSTGYQPAYTTSTTVLIQ
TTRVPKQVAVPATDTTDMQTSLDEVMTTKIIIGCFVAVTLLAAAMLIVFYKLRRHQQRS
TVTAARTVEIIQVDEDIPAATSAAATAAPSGVSGEGAVVLTPIHDHINYNTYKPAHGAHWTE
NSLGNLSLHPTVTTISEPYIIQTHTKDKVQETQI

GCTCGGGCACCAGCGCGCTGAAGATGATGAGCTGGGTGCTGGACGAGTTGGGGCTCACTTCTCTTCAGCTCC
 TTTCTCATCTGCTCTTCCGAAAGATGACACGACTTAATTAAGCGCTGCCCTGGAGCAGACTGGAAATCATGCT
 TTGCTGGGAGTGTCTGTAATATGATTCAGATTGAGTGGCTGTGGCCGGAAAGAGGGAAGTCGTGGGTTATACCAT
 CCTCTGCTGCAGAAATGAGGAGAAATGAGTGTGACTCTGCTGCTGATCCACCGAGSTGTACCAATCTTGAAGAACT
 CGAAGAGTGTCCGAAATGGCTATGGGGGGGACTCTTGATGACTCTTATGTGAAGGGGTCTACTGTGCGAGT
 TGCCGACAGCGCTGTGATCCGAGGAGACTGCATCGGATGTGGCCAGGTTTGTGCGAGGCCCGAAAGGGTCAGATT
 TTGTGAAGACTTATCCCTAATGCTCTACTGTGAATGGACCAATCATGCTAAACCTGGGTTTGTCACTCAACTA
 GATTTTGTCAATGTTGAGTCTGAAGTTTGTGACTACATGTGCGCAATGACTACTGTGAGGTCTGTGATGGAGACAG
 CGGGATGGCCGATGATCAAGGCTGTCTGTGGCAACGAGGGCCGAGCTCTATCCAGAGCATAGAGTCTCACT
 CCAGCTCTCTTTCACATCCGATGGCTCCAGAAGATTTGACGGTTTTCATCGCAATTTATAGGAGATACAGCAAT
 GCTCTCTATCCCTTTGTTTTCATGACGCCAGCTGGGCTCTTGACAAAGGCTGGAATCTTACAAGTGTGGCTGGTCTG
 CGAGGCTCTATCGGCGAGCGCTGTGAARAATCTCTTGTAAGAAGAAACTGCTCAGACCTCGGGGCGCGCTCAAT
 TGGGTACACAAAAATACAGGGGGGCTGGGCTTACAACGAGCGCAATGCTAAATTTGGCACTGGGTGTCTTT
 TCTTTTGTACAACATCTCTATGTTTATGTGTGCAATGAGAAAGAAAGTCTGGCAGCAAGATGGAGAGTGGTCAAGG
 AAAAAAGCCCTATGCATAAAAGCTGCGCAGAGAACAAAGATTTACAGCTGTGGAGAAGGAGAGTTCTTCGAT
 CGAGGTTCAGTCAAGGAGACACCAATTACACAGACTATCACTCAGCGCCCTTCAGCAAGCAGAAATCCAGAGTGT
 CCGCTACCAAGAACCGAGCCCTTCCCTTGGAGATCTGCCATGGGATACAACATCTGCATACCCAGCTCCAGT
 TATGATGTCATCTCAACCTCTTCACTCGCGCGCTGGGCAAGCAGCAGGAGCAATCTGTGAGGACTGGGAATGGAG
 TGGGGGGCACCATTCTGTCATCCCTATCTCGGGAAAGATTAGAACATCATGCTCTCAAAAGACCCAGGGTGTG
 GCTGSCCGCTGCGCAGCGAGCCATCTACAGGAGGACACGGGGGCTGCATCAGCGCAGCCTACAGCAAGGGAGCTGG
 TTTCTAGTCTCAGCGGTGCCCTGGTGAATGAGCGCACTGTGGTGGCTGCCCATGTGCTTACTGACTGGG
 GAAGTGCACCATGATCAAGACAGCAGACCTCAAGATTTGTTTGGGAAAACTTACCGGGATGATGACCGGGATG
 AAGAGACCAATCCAGAGCTACAGATTTTGTGCTATCATCTGCATCCCAATCTAGCCGATCTGCTGTGATGCT
 GACATCGCCATCTCTGAAGCTCTTACAGCAGGCGCGATACAGCAACCGGATCAGCCCATCTGCTCTGCTGCGAC
 TCGGGATCTCAGCACTCTCTCCAGGAGTCCCACTCATCTGTGGCTGGCTGGAATGTCTGCGCAGAGTGAGGA
 CGCTTGGCTTCAAGACAGCAACACTCGCTCTGGGGTGGCTCAGTGTGGTGACTCGCTGCTGTGTGAGGAGCAG
 CATGAGGACCATGGCATCCAGTGAAGTGTCACTGATAAATGATCTGTGTCGGAGCTGGGAACCACTGCGCCCTCT
 TGATATCTGCATCTCAGACAGCAGGAGGACTCGGGCTGTGCTCTTCGGGAGCAGGACATCTCTTGAGCCACGCT
 GGCACTCTGATGGGACTGGCTCAGTGGGACTATGATAAAACATCAGGACCAAGGCTTCCACTCTTCCAGCAAG
 GTGCTGCTTTTAAAGACTGGATTGAAAGAAATAAGAAATGACCAATGCTCATGCACTCTCTTGAAGAGTGTTC
 TGATATCCGCTCTAGCTGGTGTCTATGCTGGAAGCTGTGGGCTGTGAGTGTGATTTGGCTCTGAACTGG
 CTGTGCCAGGGCTCTTGACTTTCAGGCAACAAACTCAGTGAAGGGTGTGAGTACCTCTTCTGCTGTGAGGCTGAT
 CGCGCTCCCACTATAGCAGCACTAATGGAAAGTGCAGGGCTGTGACAAAGTAAAGTTTCTTCCAGAGACCC
 ATATACAAAACTCTCCACTCACTGATCGCTGGTGGTCTTCCCAACTTTCAGTTATACGAATGCCATCACTGTT
 ACAGGGGAAGCTTGGGGCTTCATGAGGCCCTTTTGAAGCTCTCAAGTTCTAGAGAGCTGCTGTGGGACAGCC
 CAGGGCAGCAGAGCTGGGATGTGGTGCATCGCTTGTGTGATCATGGCCACATACGATCTGTGCTCTTTTCTCTCC
 CCATCTCTTTGTACACATTTTAAATAAATAGGGTTGGCTTCTGAATCAAAAAAATAAAAAAATAAAAAAATA
 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA
 AAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATA

FIGURE 159

MELGCWTQLGLTFLQLLLISSLPREYTVINEACPGAENIMCRECCEYDQIECVCPGKREVV
GYTIPCCRNEENECDSCLIHPGCTIFENCKSCRNGSWGGLDDFYVKGIFYCAECRAGWYGGD
CMRCGQVLRAPKGQILLESYPLNAHCEWTIHAKPGFVIQLRFVMLSLEFDYMCQYDYVEVRD
GDNRDGGQIIKRVCGNERPAPIQSIGSSLHVLHSDGSKNFDGFHAIYEEITACSSSPCFHDG
TCVLDKAGSYKCACLAGYTGRCENLLEERNCSDPGGPVNGYQKITGGPGLINGRHAKIGTV
VSFFCNNSYVLSGNEKRTCQQNGEWSGKQPICIKACREPKISDLVRRRVLPMPQVQSRETPLH
QLYSAAFSKQLQSAPTCKKPALPFGDLPMGYQHLHTQLQYECISPFYRRLGSSRRTCLRTGK
WSGRAPSCIPICGKIENITAPKTQGLRWPQAAIYRRTSGVHDGSLHKGAWFLVCSGALVNE
RTVVVAAHCVTDLGKVTMIKTADLKVVLGKFYRDDDRDEKTIQSLQISAIILHPNYDPILLD
ADIAIILKLLDKARISTRVQPICLAASRDLSTSFQESHITVAGWNVLADVRSPGFKNLTLRSG
VVSVDLSLLCEEQHEDHGIPVSVTDNMFCASWEPTAPSDICTAETGGIAAVSFPGRASPEPR
WHLMGLVSWSYDKTCSHRLSTAFTKVLPFKDWIERNMK

FIGURE 160

ACCAGGCATTGTATCTTCAGTTGTCATCAAGTTCGCAATCAGATTGGAAAAGCTCAACTTGA
 AGCTTTCTTGCTGCACTGAAGCAGAGAGATAGATATTATTCACGTAATAAAAAACATGGGC
 TTCAACCTGACITTTCCACCTTTCTCTACAAATTCGATTACTGTTGCTGTTGACTTTGTGCCT
 GACAGTGGTTGGGTGGGCCACCACTAACTACTTCGTGGGTGCCATTCAAGAGATTCCCTAAAG
 CAAAGGAGTTCATGGCTAATTTCCATAAGACCCTCATTTTGGGGAAGGGAAAAACTCTGACT
 AATGAAGCATCCACGAAGAAGGTAGAAGTTGACAAGTGTCTTCTGTGCTCCTTACCTCAG
 AGGCCAGAGCAAGCTCATTTTCAAACCAGATCTCACTTTGGAAGAGGTACAGGCAGAAAATC
 CCAAAGTGTCCAGAGGCCGGTATCGCCCTCAGGAATGTAAAGCTTTACAGAGGGTCGCCATC
 CTCGTTCCCCACCGAACAGAGAGAAACACCTGATGTACCTGCTGGAACATCTGCATCCCTT
 CCTGCAGAGGCAGCAGCTGGATTATGGCATCTACGTCATCCACCAGGCTGAAGGTAAAAAGT
 TTAATCGAGCCAACTCTTGAATGTGGCTATCTAGAAGCCCTCAAGGAAGAAAATTGGGAC
 TGCTTTATATTCCACGATGTGGACCTGGTACCCGAGAATGACTTTAACCTTTACAAGTGTGA
 GGAGCATCCCAAGCATCTGGTGGTTGGCAGGAACAGCACTGGGTACAGGTTACGTTACAGTG
 GATATTTTGGGGGTGTTACTGCCCTAAGCAGAGAGCAGTTTTTCAAGGTGAATGGATTCTCT
 AACAACTACTGGGGATGGGGAGGCCAAGACGATGACCTCAGACTCAGGGTTGAGCTCCAAG
 AATGAAAATTTCCCGCCCTGCCTGAAGTGGGTAATAATACAATGGTCTTCCACACTAGAG
 ACAAGGCAATGAGGTGAACGACGAGATGAAGCTCTTACACCAAGTGTACGAGTCTGG
 AGAACAGATGGGTGAGTAGTTGTCTTATAAAATTAGTATCTGTGGAACACAATCCTTTATA
 TATCAACATCACAGTGGATTTCTGGTTTGGTGCATGACCCTGGATCTTTTGGTGATGTTTGG
 AAGAAGTATTCTTTGTTTGAATAATTTTGGCCTAGAGACTTCAAATAGTAGCACACATTA
 AGAACCTGTTACAGCTCATTTGTTGAGCTGAATTTTTCCCTTTTGTATTTTCTTAGCAGAGCT
 CCTGGTGATGTAGAGTATAAACAGTTGTAAACAAGACAGCTTTCTTAGTCATTTTGATCATG
 AGGGTTAAATATTGTAATATGGTACTTGAAGGACTTTATATAAAAGGATGACTCAAAGGAT
 AAAATGAACGCTATTTGAGGACTCTGGTTGAAGGAGATTTATTTAAATTTGAAGTAATATAT
 TATGGGATAAAAGGCCACAGGAATAAGACTGCTGAATGTCTGAGAGAACCAAGTGTGTCT
 CGTCCAAGGTAGAAAGGTACGAAGATACAATACTGTTATTTCATTATCCTGTACAAATCATCT
 GTGAAGTGGTGGTGTGAGGTGAGAAGGCGTCCACAAAAGAGGGGAGAAAAGGCGACGAATCA
 GGACACAGTGAAGTTGGGAATGAAGAGGTAGCAGGAGGGTGGAGTGTGCGGTGCAAGGCAG
 CAGTAGCTGAGCTGGTTGCAGGTGCTGATAGCCTTCAGGGGAGGACCTGCCAGGTATGCCT
 TCCAGTGATGCCACCAGAGAATACATTCTCTATTAGTTTTTAAAGAGTTTTTGTAAAAATGA
 TTTTGTACAAGTAGGATATGAATTAGCAGTTTACAAGTTTACATATTAACATAATAATAATA
 TGTCTATCAAATACCTCTGTAGTAAAAATGTGAAAAGCAAAA

FIGURE 161

MGFNLT FHL SYKFRLLLLLTLC LTVVGWATS NYFVGAIQEIPKAKEFMANFHKT LILGKGKT
LTNEASTKKVELDNCP SVSPYL RGQSKLIFKPDLTLEE VQAENPKVSRGRYRPQECKALQRV
AILVPHRNR EKHLMYLLEHLHPFLQRQQLDYGIYVIHQAE GKKFNRAKLLNVGYLEALKEEN
WDCFI FHDVDLVPENDFNLYKCEEHPKHLVVGRNSTGYRLRYSGYFGGV TALSREQFFKVNG
FSNNYWG WGGEDDDLRLRVELQRMKISRPLPEVGK YTMVFHTRDKGNEVNAERMKLLHQVSR
VWR TDGLSSCSYKLV SVEHNPLYINITVDFWFGA

Important features:**Signal peptide:**

amino acids 1-27

N-glycosylation sites:

amino acids 4-7, 220-223 and 335-338

Xylose isomerase proteins:

amino acids 191-201

FIGURE 162

CGTGGGCCGGGGTCGCGCAGCGGGCTGTGGGCGCGCCGGAGGAGCAGCCGCCGAGTTCTC
 GAGCTCCAGCTGCATTCCCTCCGCGTCCGCCCCACGCTTCTCCCGCTCCGGGCCCGCGCAATG
 GCCCAGGCAGTGTGGTCGCGCCTCGGCCGCATCCTCTGGCTTGCTTGCTCCTGCCCTGGGC
 CCCGCGAGGGGTGGCGCAGGCCTGTATGAACCTCAATCTCACACCGTAGCCCTGCGCCACCA
 CGGGAGCGGTGGTGACCATCTCGGCCAGCCTGGTGGCCAAGGACAACGGCAGCCTGGCCCTG
 CCCGCTGACGCCACCTCTACCGCTTCCACTGGATCCACACCCCGCTGGTGCTTACTGGCAA
 GATGGAGAAGGGTCTCAGCTCCACCATCCGTGTGGTCGGCCACGTGCCCGGGGAATTCCTCG
 TCTCTGTCTGGGTCACTGCCGCTGACTGCTGGATGTGCCAGCCTGTGGCCAGGGGCTTTGTG
 GTCCTCCCATCACAGAGTTCTCGTGGGGGACCTTGTGTGTCACCCAGAACACTTCCCTACC
 CTGGCCCAGCTCCTATCTCACTAAGACCGTCTGAAAGTCTCCTTCCCTCCACGACCCGA
 GCAACTTCTCAAGACCGCCTTGTCTCTACAGCTGGGACTTGGGGACGGGACCCAGATG
 GTGACTGAAGACTCCGTGGTCTATTATAACTATTCCATCATCGGGACCTTACCGTGAAGCT
 CAAAGTGGTGGCGAGTGGGAAGAGGTGGAGCCGGATGCCACGAGGGCTGTGAAGCAGAAGA
 CCGGGGACTTCTCCGCGCTCGCTGAAGCTGCAGGAACCCCTTCGAGGCACTCCAAGTGTGGGG
 CCCACCTTAATTCAGACCTTCCAAAAGATGACCGTGACCTTGAACCTTCTGGGGAGCCCTCC
 TCTGACTGTGTGCTGGCGTCTCAAGCCTGAGTGCCCTCCCGCTGGAGGAAGGGGAGTGCCACC
 CTGTGTCCGTGGCCAGCACAGCGTACAACCTGACCCACACCTTTCAGGGACCTGGGGACTAC
 TGCTTCAGCATCCGGGCGCGAGAATATCATCAGCAAGACACATCAGTACCAAGAATCCAGGT
 GTGGCCCTCCAGAATCCAGCCGGCTGTCTTTGCTTTCCCATGTGCTACACTTATCACTGTGA
 TGTGGCCCTTCATCATGTACATGACCCCTGCGGAATGCCACTCAGCAAAAGGACATGGTGGAG
 AACCCGGAGCCACCTCTGGGGTCAAGTGTGCTGCTGCCAGATGTGCTGTGGGCCCTTCTGTGCT
 GGAGACTCCATCTGAGTACCTGGAAATGTGTCGTGAGAACACGGGGCTGCTCCCGCCCCCTCT
 ATAAGTCTGTCAAACTTACACCGTGTGAAGCACTCCCCCTCCCCACCCCATCTCAGTGTATA
 CTGACTGTGACTTGGAGTTTCCAGCAGGGTGGTGTGCACCACTGACCAGGAGGGGTTCATT
 TGCGTGGGGCTGTTGGCCTGGATCATCCATCCATCTGTACAGTTGACCCACTGCCACAAGCC
 CCTCCCTCTGTGCACCCCGACCCCGACCATTCACCCATCTGTACAGTCCAGCCACTGACA
 TAAGCCCCACTCGGTTACACCCCTTACCCCTACCTTTGAAGAGGCTTCGTGCAGGACT
 TTGATGCTTGGGGTGTCCGTGTGACTCCTAGGTGGGCTTGCTGCCACTGCCCATTCCT
 CTCATATTGGCACATCTGCTGTCCATTGGGGTCTCAGTTTCTCCCCAGACAGCCCTAC
 CTGTGCCAGAGAGCTAGAAGAAGGTATAAAGGGTTAAAAATCCATAACTAAAGGTGTGAC
 ACATAGATGGGCACACTCAGAGAGAGAAGTGTGCATGTACACACACACACACACACACACA
 CACACACACACAGAAATATAAACACATGCGTCACATGGGCATTTCAGATGATCAGCTCTGTA
 TCTGGTTAAGTGGTGTGCTGGGATGCACCTGCACCTAGAGCTGAAAGGAAATTTGACCTCCA
 AGCAGCCCTGACAGGTTCTGGGCCGGGCCCTCCCTTTGTGCTTGTCTCTGCAAGTTCTTGC
 GCCCTTTATAAGGCCATCTAGTCCCTGCTGGCTGGCAGGGGCTGGATGGGGGGCAGGACT
 AATACTAGTGATGACAGAGTGTCTTATAAATATCACCTTATTTTATGAAACCCATCTGTG
 AAACCTTCACTGAGGAAAAGGCCCTTGCAGCGGTAGAAGAGGTTGAGTCAAGGCCGGGCGCG
 TGGCTCACGCCTGTAATCCAGCACTTTGGGAGGCCGAGGCGGGTGGATCACGAGATCAGGA
 GATCGAGACCACTCCGCTAACACCGGTGAACCCCGTCTCTACTAAAAAATACAAAAAGTT
 AGCCGGGCGTGGTGGTGGGTGCTGTAGTCCAGCTACTCGGGAGGCTGAGGCAGGAGAAATG
 GTGCGAACCCGGGAGCGGAGCTTGTCAGTGAGCCAGATGGCGCCACTGCCTCCAGCCTGA
 GTGACAGAGCGAGACTCTGTCTCCA

FIGURE 163

MAQAVWSRLGRILWLACLLPWAPAGVAAGLYELNLTTDSPATTGAVVTISASLVAKDNGSLA
 LPADAHLYRFHWIHTPLVLTGKMEKGLSSTIRVVGHVPGEFPVSVVWTAADCWMCQPVARGF
 VVLPITEFLVGLDVVTQNTSLPWPSYLTKTVLKVSFLLHDPNFKLTALFLYSWDFGDTGQ
 MVTEDSVVYNYNSIIIGTFTVKLVVAEWEEVEPDATRAVKQKTGDFSASLKLQETLRGIQVL
 GPTLIQTFQKMTVTLNFLGSPPLTVCWRLKPECLPLEEGECHPVSVASTAYNLTHTRDPGD
 YCFSIRAENIIISKTHQYHKIQVWPSRIQPAVFAFPCATLITVMLAFIMYMTLRNATQQKDMV
 ENPEPPSGVRCCCMCCGPFLLETPSEYLEIVRENHGLLPPLYKSVKTYTV

Important features of the protein:**Signal peptide:**

amino acids 1-24

Transmembrane domain:

amino acids 339-362

N-glycosylation sites.

amino acids 34-37, 58-61, 142-145, 197-200, 300-303 and 364-367

FIGURE 164

GCTCAAGACCCAGCAGTGGGACAGCCAGACAGACGGCACGATGGCACTGAGCTCCCAGATCT
 GGGCCGCTTGCCCTCCTGCTCCTCCTCCTCCTCGCCAGCCTGACCAGTGGCTCTGTTTTCCCA
 CAACAGACGGGACAACTTGCAGAGCTGCAACCCAGGACAGAGCTGGAGCCAGGGCCAGCTG
 GATGCCCATGTTCCAGAGGCGAAGGAGGCGAGACACCCACTTCCCATCTGCATTTTCTGCT
 GCGGCTGCTGTCATCGATCAAAGTGTGGGATGTGCTGCAAGACGTAGAACCTACCTGCCCTG
 CCCCCGTCCCCTCCCTTCCCTTATTTATTCCTGCTGCCCCAGAACATAGGTCTTGGAATAAAA
 TGGCTGGTTCTTTTGTTCCTTTCCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AAA

FIGURE 165

MALSSQIWAACLLLLLLLLSLTSGSVFPQQTGQLAELQPQDRAGARASWMPMFQRRRRRDTH
FPICIFCCGCCHRSKCGMCCKT

165/330

FIGURE 166

CTGTCAGGAAGGACCATCTGAAGGCTGCAATTGTGTTCTTAGGGAGGCAGGTGCTGGCCTGGC
 CTGGATCTTCCACC**ATG**TTTCCTGTGTGCTGCCTTTTGATAGCCTGATTGTCAACCTTCTGGGC
 ATCTCCCTGACTGTCTCTTCCACCTCCTTCTCGTTTTTCATCATAGTGCACGCCATTTTTGG
 AGTCTCCTTTGGTATCCGCAAACTCTACATGAAAGTCTGTTAAAACTTTGGCTGGGCTA
 CCTTGAGAATGGAGCGAGGAGCCAAGGAGAAGAACCACAGCTTTACAAGCCCTACACCAAC
 GGAATCATTTGCAAGGATCCCACTTCACTAGAAGAAGAGATCAAGAGAGATTCTGTCGAAGTGG
 TAGTAGTAAGGCTCTGGACAACACTCCAGAGTTCGAGCTCTCTGACATTTTCTACTTTTGGC
 GGAAGGAATGGAGACCATTATGGATGATGAGGTGACAAGAGATTCTCAGCAGAAGAACTG
 GAGTCTTGGAACTGCTGAGCAGAACCAATTATAACTTCCAGTACATCAGCCTTCGGCTCAC
 GGTCTCTGTGGGGTTAGGAGTGTGATTTCGGTACTGCTTTCTGCTGCCCTCAGGATAGCAC
 TGGCTTTTACAGGGATTAGCCTTCTGGTGGTGGGCACAACGTGGTGGGATCTTGCCAAAT
 GGGAGGTTTAAGGAATTCATGAGTAAACATGTTCACTTAATGTGTACCGGATCTGCGTGCG
 AGCGCTGACAGCCATCATCACCTACCATGACAGGGAACAGACCAAGAAATGGTGGCATCT
 GTGTGGCCAAATCATACCTCACCAGTCGATGTGATCATCTTGGCCAGCGATGGCTATTATGCC
 ATGGTGGGTCAAGTGCACGGGGGACTCATGGGTGTGATTACAGAGACCATGGTGAAGGCTG
 CCCACACGCTCTGGTTTGAGCGCTCGGAAGTGAAGGATCGCCACCTGGTGGCTAAGAGACTGA
 CTGAACATGTGCAAGATAAAAGCAAGCTGCCATCTCTCATCTTCCAGAAGGAACCTGCATC
 AATAATACATCGGTGATGATGTTCAAAAAGGGAAGTTTTGAAATTTGGAGCCACAGTTTTACCC
 TGTGTCTATCAAGTATGACCCCTCAATTTGGCGATGCCCTTCTGGAACAGCAGCAAAATACGGGA
 TGGTGACGTACCTGCTGCGAATGATGACCAGCTGGGCGATTGTCTGCAGCGTGTGGTAGCTG
 CCTCCCATGACTAGAGAGGCAGATGAAGATGCTGTCCAGTTTGGCAATAGGGTGAATCTGC
 CATTGGCAGGCAGGGAGGACTTGTGGACCTGCTGTGGGATGGGGGCCCTGAAGAGGGAGAAGG
 TGAAGGACACGTTCAAGGAGGAGCAGCAGAAGCTGTACAGCAAGATGATCGTGGGGAACCA
 AAGGACAGGAGCGCTCTCT**TGA**GCCTGCCAGCTGGCTGGGGCCACCGTGCGGGGTGCCAA
 CGGGCTCAGAGCTGGAGTTGCCGCCGCCGCCCCACTGCTGTGTCTTTCCAGACTCCAGGG
 CTCGCCGGGCTGCTCTGGATCCCAGGACTCCGGCTTTCGCCAGAGCCGACGCGGGATCCCTGT
 GCACCCGGCGCAGCCTACCTTGGTGGTCTAAACGGATGCTGCTGGGTGTTGCGACCCAGGA
 CGAGATGCTTTGTTCTTTTACAATAAGTCTGTGGAGGAATGCCATTAAAGTGAACCTCCCA
 CCTTTGCAACGCTGTGCGGGCTGAGTGGTTGGGGAGATGTGGCCATGGTCTTGTGCTAGAGAT
 GGGCGTACAAGAGTCTGTTATGCAAGCCCGTGTGCCAGGGATGTGCTGGGGGGGCCACCCG
 CTCTCCAGGAAGGCACAGCTGAGGCACTGTGGCTGGCTTCGGCCTCAACATCGCCCCAGC
 CTTGGAGCTCTGCAGACATGATAGGAAGGAACTGTCACTGACAGGGGCTTTCAGCAAAATG
 AAGGGTTAGATTTTATGCTGCTGCTGATGGGTTACTAAAGGAGGGGGAAGAGGGCAGGTG
 GGCCGCTGACTGGGCCATGGGGAGAACGTGTGTTCGTACTCCAGGCTAACCTGAACTCCCC
 ATGTGATGCGCGCTTTGTTGAATGTGTGCTCGGTTTCCCATCTGTAATATGAGTCGGGGG
 GAATGGTGGTATTCCTACCTCACAGGCTGTGTGGGATTAAGTGTGCGGGTGTGAGTGA
 AGGACACATCAGTTCAGTGTTCAGTACAGGCCACAAACGGGGCACGGCAGCCCTGAG
 CTCAGAGCTGCTGCACTGGGCTTTGGATTGTTCTTGTGAGTAAATAAACTGGCTGGTGAA
 TGA

FIGURE 167

MFLLLPFD SLIVNLLGISLTVLFTLLLVFIIVPAIFGVSF GIRKLYMKSLLKIFAWATLRME
 RGAKEKNHQLYKPYTNGITAKDPTSLEEEIKEIRRS GSSKALDNTPEFELSDIFYFCRKGME
 TIMDDEVTKRFSAAEELSWNLLSRTNYNFQYISLRLTVLWGLGVLI RYCFLPLRLIALAFTG
 ISLLVVGTTVVGYLPNGRFKEFMSKHVHLMCYRICVRALTAIITYHDRENRP RGGICVANH
 TSPIDV IILASDGY YAMVGQVHGGLMGVIQRAMVKACPHVWFERSEVKDRHLVAKRLTEHVQ
 DKSKLPILIFPEGTCINNTSVM MFKKSFEIGATVYPVAIKYDPQFGDAFWNSSKYGMV TYL
 LRMMTSWAIVCSVWYLP PMTREADED AVQFANRVKSAIARQGG LVDLLWDGGLKREKV KDTF
 KEEQQKLYSKMIVGNHKDRSRS

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FIGURE 168

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 C G A T A C C T A T G T G G G T T G T G C A G A G G A T G G A G G A A G G C A G C C C C C T G C T A A A G G A G G
 A A A T G G C C C A C C A T G C C C T G C T G C G G G A A T C C T G G G A G G C A G C C C A G G A G A C C T G G G A G G A C
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 G C T C C C G G G A G C T C T A C A T G A G G C A C T T T C C C T T C A A G G C C C T G C A T T T C T A C C T G A T C C G G
 G C C C T G C A G C T G C T G C G A G G C A G T G G G G G C T G C A G C A G G G G A C C T G G G G A G G T G G T G T T C C G
 A G G T G T G G G C A G C C T T C G C T T T G A A C C C A A G A G G C T G G G G G A C T C T G T C C G C T T G G G C C A G T
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 G T G T C T G C C C A G G G G T G C A G C T A G G G T C A C A A T C T G A G G G G G C C T C C T C T C T G C C C C C C T G
 G A A G A C T C T G C T C T T G G C C C C T G G A G A G T T C C A G C T C T C A G G G G T T G G G C C C **T G A** A A G T C C A
 A C A T C T G C C A C T T A G G A G C C C T G G G A A C G G G T G A C C T T C A T A T G A C G A A G A G G C A C C T C C A G
 C A G C C T T G A G A A G C A A G A A C A T G G T T C C G G A C C C A G C C C T A G C A G C C T T C T C C C C A A C C A G G
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MALAALMIALGSLGLHTWQAQAVPTILPLGLAPDTFDDTYVVGCAEEMEKAAPLLKEEMAHH
 ALLRESWEAAQETWEDKRRGLTLPFGFKAQNGIAIMVYTNSSNTLYWELNQAVRTGGGSRRL
 YMRHFPFKALHFYLIRALQLLRGSGGCSRGPGEVFRVGVSLRFEPKRLGDSVRLQGFASS
 LDKAVAHRFGEKRRGCVSAPGVQLGSQSEGASSLPWKTLTLLAPGEFQLSGVGP

FIGURE 170

GTGGCTTCATTTTCAGTGGCTGACTTCCAGAGAGCAAT**ATGG**CTGGTTCCTCCCAACATGCCTCA
 CCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCCTCTGGACCCGTGAAAGAGCTG
 GTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTCCAAAGTAAAGCAAGTTGACTC
 TATTGCTGAGACCTTCAACACAACCCCTCTTGTCAACATACAGCCAGAAGGGGGCACTATCA
 TAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCAGATGGAGGCTACTCCCTGAAG
 CTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGTGGGGATATACAGCTCATCACT
 CCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACGAGCACCTGTCAAAGCCTAAAG
 TCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTGACCAATCTGACATGCTGCATG
 GAACATGGGGAAGAGGATGTGATTTTATACCTGGAAGGCCCTGGGGCAAGCAGCCAAATGAGTC
 CCATAATGGGTCCATCCTCCCATCTCCTGGAGATGGGGAGAAAGTGATATGACCTTCATCT
 GCGTTGCCAGGAACCCCTGTGAGCAGAACTTCTCAAGCCCCATCCTTGCCAGGAAGCTCTGT
 GAAGGTGCTGCTGATGACCCAGATTCCATGGTCTCCTGTGTCTCCTGTTGGTGCCCTT
 CCTGCTCAGTCTCTTTGTACTGGGGCTATTTCTTTGGTTTCTGAAGAGAGAGAGACAAGAAG
 AGTACATTGAAGAGAAGAAGAGAGTGGACATTTGTGCGGGAACCTCCTAACATATGCCCCAT
 TCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAATAGAACAACTCCTAAAGGAAGA
 TCAGCAAATACGGTTTACTCCACTGTGGAATACCGAAAAAGATGGAAAATCCCCACTCAC
 TGCTCAGATGCCAGACACCAAGGCTATTTGCCTATGAGAATGTTATC**TAG**ACAGCAGTG
 CACTCCCCTAAGTCTCTGCTCA

FIGURE 171

MAGSPTCLTLIYILWQLTGSAAAGPVKELVGSVGGAVTFPLKSKVKQVDSIVWTFNTTPLVT
 IQPEGGTIIVTQNRNRERVDFFPDGGYSLKLSKLKKNDSGIYYVGIYSSSLQQPSTQEYVLHV
 YEHLSPKPVMTGLQSNKNGTCVTNLTCCMEHGEEVDVIYTWKALGQAANESHNGSILPISWRW
 GESDMTFICVARNPVSARNFSSPILARKLCEGAADDPSSMVLLCLLLVPLLLSLFLGLFLW
 FLKRERQEEYIEKKRVDICRETPNICPHSGENTEYDTIPHTNRTILKEDPANTVYSTVEIP
 KKMENPHSLLTMPDTPRLFAYENVI

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FIGURE 172

CTGGTTCCCCAACATGCCTCACCCCTCATCTATATCCTTTGGCAGCTCACAGGGTCAGCAGCC
TCTGGACCCGTGAAAGAGCTGGTCGGTTCCGTTGGTGGGGCCGTGACTTTCCCCCTGAAGTC
CAAAGTAAAGCAAGTTGACTCTATTGTCTGGACCTTCAACACAACCCCTCTTGTCAACATAC
AGCCAGAAGGGGGCCTATCATAGTGACCCAAAATCGTAATAGGGAGAGAGTAGACTTCCCA
GATGGAGGCTACTCCCTGAAGCTCAGCAAACCTGAAGAAGAATGACTCAGGGATCTACTATGT
GGGGATATACAGCTCATCACTCCAGCAGCCCTCCACCCAGGAGTACGTGCTGCATGTCTACG
AGCACCTGTCAAAGCCTAAAGTCACCATGGGTCTGCAGAGCAATAAGAATGGCACCTGTGTG
ACCAATCTGACATGCTGCATGGAACATGGGGAAGAGGATGTGATTTATACCTGGAAGGCCCT
GGGGCAAGCAGCCAATGAGTCCCATAAATGGGTCCATCCTCCCCATCTCCTGGAGATGGGGAG
AAAGTGATATGACCTTCATCTGCGTTGCCAGGAACCCCTGTCAGCAGAACTTCTCAGCCCC
ATCCTTGCCAGGAAGCTCTGTGAAGGTGCTGCTGATGACCCAGATTCCCTCCATGGTCTCCT
GTGTCTCCTGTTGGTGCCCTCCTGCTCAGTCTCTTTGTACTGGGGCTATTCTTTTGGTTTC
TGAAGAGAGAGAGACAAGAAGAGTACATTGAAGAGAAGAAGAGAGTGGACATTGTGCGGAA
ACTCTAACATATGCCCCATTCTGGAGAGAACACAGAGTACGACACAATCCCTCACACTAA
TAGAACATCCTAAAGGAAGATCCAGCAATACGGTTTACTCCACTGTGGAAATACCGAAAA
AGATGGAAAAATCCCCACTCACTGCTCACGATGCCAGACACCAAGGCTATTGCTATGAG
AATGTTATCTAGACAGCAGTGCCTCCCTAAGTCTCTGCTCAAAAAAAAAAAAAAAAAAAAA

FIGURE 173

GAAAGACGTGGTCCTGACAGACAGACAATCCTATTCCCTACCAAAATGAAGATGCTGCTGCT
GCTGTGTTGGGACTGACCCCTAGTCTGTGTCCATGCAGAAGAAGCTAGTTCTACGGGAAGGA
ACTTTAATGTAGAAAAGATTAAATGGGGAATGGCATACTATTATCCTGGCCTCTGACAAAAGA
GAAAAGATAGAAGAACATGGCAACTTTAGACTTTTTCTGGAGCAAATCCATGTCTTGGAGAA
TTCCTTAGTTCTTAAAGTCCATACTGTAAGAGATGAAGAGTGCTCCGAATTATCTATGGTTG
CTGACAAAACAGAAAAGGCTGGTGAATATTCTGTGACGTATGATGGATTCAATACATTTACT
ATACCTAAGACAGACTATGATAACTTTCTTATGGCTCACCTCATTAAACGAAAAGGATGGGGA
AACCTTCAGCTGATGGGGCTCTATGGCCGAGAACCAGATTTGAGTTCAGACATCAAGGAAA
GGTTTGCAACTATGTGAGGAGCATGGAATCCTTAGAGAAAATATCATTGACCTATCCAAT
GCCAATCGCTGCCTCCAGGCCGAGAATGAAGAATGCCTGAGCCTCCAGTGTTGAGTGGAC
ACTTCTCACCAGACTCCACCATCATCCCTTCCTATCCATACAGCATCCCAGTATAAATTC
TGTGATCTGCATTCCATCCTGTCTCACTGAGAAGTCCAATCCAGTCTATCAACATGTTACC
TAGGATACCTCATCAAGAATCAAAGACTTCTTTAAATTTCTCTTTGATACACCCTTGACAAAT
TTTTTCATGAAATTATTCCTCTTCTGTTCAATAAATGATTACCTTGCACTTAA

FIGURE 175

GGCTCGAGCGTTTCTGAGCCAGGGGTGACCATGACCTGCTGCGAAGGATGGACATCCTGCAA
TGGATTTCAGCCTGCTGGTTCTACTGCTGTTAGGAGTAGTTCTCAATGCGATACCTCTAATTG
TCAGCTTAGTTGAGGAAGACCAATTTTCTCAAAACCCATCTCTTGCTTTGAGTGGTGGTTC
CCAGGAATTATAGGAGCAGGTCTGATGGCCATTCCAGCAACAACAATGTCCTTGACAGCAAG
AAAAAGAGCGTGCTGCAACAACAGAACTGGAATGTTTCTTTCATCATTTTTTCAGTGTGATCA
CAGTCATTGGTGCTCTGTATTGCATGCTGATATCCATCCAGGCTCTCTTAAAAGGTCCTCTC
ATGTGTAATTCTCCAAGCAACAGTAATGCCAATTGTGAATTTTCATTGAAAAACATCAGTGA
CATTTCATCCAGAATCCTTCAACTTGCACTGGTGGTGGTGGTGGGAGGAGCATCTAGTTTCCAC
TTCGATTCTGAAGAAAACAACATAGGCTTATCCACTTCTCAGTATTTTGGGTCTATTGCT
TGTTGGAATTCTGGAGGTCCTGTTGGGCTCAGTCAGATAGTCATCGGTTTCTTGGCTGTC
TGTTGGAGTCTCTAAGCGAAGAAGTCAAATTGTGTAGTTTAATGGGAATAAAATGTAAGTA
TCAGTAGTTTGAAAAAAAAA

FIGURE 176

MTCCGWTSCNGFSLVLVLLLLGVVLNAIPLIVSLVEEDQFSQNPISCFEWWFPGIIGAGLMA
IPATTMSLTARKRACCNRTGMFLSSFFSVITVIGALYCM LISIQALLKGPLMCNSPSNSNA
NCEFSLKNISDIHPESFNLQWFFNDSCAPPTGFNKPTSNDTMASGWRASSFHF DSEENKHRL
IHFSVFLG LLLVGILEVLFGLSQIVIGFLGCLCGVSKRRSQIV

FIGURE 177

GTGGAATCCAAATCACTCATTTGTGAAAGCTGAGCTCACAGCCGAATAAGCCACCATGAGGCT
GTCAGTGTGTCTCCTGATGGTCTCGCTGGCCCTTTGCTGCTACCAGGCCCATGCTCTTGTCT
GCCCAGCTGTTGCTTCTGAGATCACAGTCTTCTTATTCTTAAGTGACGCTGCGGTAAACCTC
CAAGTTGCCAAACTTAATCCACCTCCAGAAGCTCTTGACGCCAAGTTGGAAGTGAAGCACTG
CACCGATCAGATATCTTTTAAGAAACGACTCTCATTGAAAAAGTCCTGGTGGAAATAGTGAA
AAAATGTGGTGTGTGACATGTAAAAATGCTCAACCTGGTTTCCAAAGTCTTTCAACGACACC
CTGATCTTCACTAAAAATTGTAAAGGTTTCAACACGTTGCTTTAATAAATCACTTGCCCTGC

178/330

FIGURE 178

MRLSVCLLMVSLALCCYQAHALVCPAVASEITVFLFLSDAAVNLQVAKLNPPPEALAAKLEV
KHCTDQISFKRRLSLKKSWWK

178/330

FIGURE 179

ATCCGTTCTCTGCGCTGCCAGCTCAGGTGAGCCCTCGCCAAGGTGACCTCGCAGGACACTGG
TGAAGGAGCAGTGAGGAACCTGCAGAGTCACACAGTTGCTGACCAATTGAGCTGTGAGCCTG
GAGCAGATCCGTGGGCTGCAGACCCCGCCCCAGTGCCCTCTCCCCCTGCAGCCCTGCCCTC
GAACTGTGACATGGGAGAGAGTGACCCCTGGCCCTTCTCCTACTGGCAGGCCTGACTGCCTTGG
AAGCCAATGACCCATTGCCAATAAAGACGATCCCTTCTACTATGACTGGAAAAACCTGCAG
CTGAGCGGACTGATCTGCGGAGGGCTCCTGGCCATTGCTGGGATCGCGGCAGTTCTGAGTGG
CAAATGCAAATACAAGAGCAGCCAGAAGCAGCACAGTCTGTACCTGAGAAGGCCATCCCAC
TCATCACTCCAGGCTCTGCCACTACTTGCTTGAGCACAGGACTGGCCTCCAGGGATGGCCTGA
AGCCTAACACTGGCCCCCAGCACCTCCTCCCCTGGGAGGCCTTATCCTCAAGGAAGGACTTC
TCTCCAAGGGCAGGCTGTTAGGCCCTTTCTGATCAGGAGGCTCTTTATGAATTAACTCG
CCCCACCACCCCTCA

180/330

FIGURE 180

MERVTLALLLLAGLTALEANDPFANKDDPFYYDWKNLQLSGLICGGLLAIAGIAAVLSGKCK
YKSSQKQHSPVPEKAIPILITPGSATTC

180/330

FIGURE 181

GGAGAAGAGGTTGTGTGGGACAAGCTGCTCCCGACAGAAGG**ATG**TCGCTGCTGAGCCTGCC
 TGGCTGGGCCTCAGACCGTGGCAATGTCCCATGGCTACTCCTGCTGCTGGTTGTGGGCTC
 CTGGCTACTCGCCGCATCCTGGCTTGGACCTATGCCTTCTATAACAAGTCCCGCGGCTCC
 AGTGTTTCCACAGCCCCCAAACGGAACTGGTTTTGGGGTCACCTGGGCCTGATCACTCCT
 ACAGAGGAGGGCTTGAAGGACTCGACCCAGATGTGGGCCACCTATCCAGGGCTTTACGGT
 ATGGCTGGGTCCCATCATCCCTTCATCGTTTTATGCCACCTGACACCATCCGGTCTATCA
 CCAATGCCTCAGCTGCCATTGCACCCAAGGATAATCTCTTCATCAGGTTCTGGAAGCCCTGG
 CTGGGAGAAGGGATACTGTGAGTGGCGGTGACAAGTGGAGCCGCCACCGTCGGATGCTGAC
 GCCCGCCTTCATTCAACATCCTGAAGTCTATATAACGATCTTCAACAAGAGTGCAAACA
 TCATGCTTGACAAGTGGCAGCACCTGGCCTCAGAGGGCAGCAGTCGTCTGGACATGTTTGAG
 CACATCAGCCTCATGACCTTGGACAGTCTACAGAAATGCATCTTCAGCTTTGACAGCCATTG
 TCAGGAGAGGGCCAGTGAATATATTGCCACCATCTTGGAGCTCAGTGCCCTTGTAGAGAAAA
 GAAGCCAGCATATCCTCCAGCACATGGACTTCTGTATTACCTCTCCCATGACGGGCGGCGC
 TTCCACAGGGCCTGCCGCCCTGGTGCATGACTTTCACAGACGCTGTATCCGGGAGCGGCGTCG
 CACCTCCCCACTCAGGATATTGATGATTTTTTCAAAGACAAAGCCAAGTCCAAGACTTTGG
 ATTTTCATTGATGTCTTCTGCTGAGCAAGGATGAAGATGGGAAGGCATTGTGATGAGGAT
 ATAAGAGCAGAGGCTGACACCTTCATGTTTGGAGGCCATGACACCACGGCCAGTGGCCTCTC
 CTGGGTCTGTACAACCTTGCGAGGCACCCAGAATACCAGGAGCGCTGCCGACAGGAGGTGC
 AAGAGCTTCTGAAGGACCGCGATCCTAAAGAGATTGAATGGGACGACCTGGCCAGCTGCC
 TTCTGACCATGTGCGTGAAGGAGAGCCTGAGGTTACATCCCCAGCTCCCTTCATCTCCCG
 ATGCTGCAACCCAGGACATTGTTCTCCAGATGGCCGAGTCATCCCCAAAGGCATTACCTGCC
 TCATCGATATTATAGGGGTCCATCACAACCCAACCTGTGTGGCCGATCCTGAGGTCTACGAC
 CCCTTCGCTTTGACCCAGAGAACAGCAAGGGGAGGTACCTCTGGCTTTTATTCTTTCTC
 CGCAGGGCCAGGAATGCATCGGGCAGGCGTTGCCATGGCGGAGATGAAAGTGGTCTTGG
 CGTTGATGCTGCTGCACTTCCGGTTCCTGCCAGACCACTGAGCCCCGAGGAAGCTGGAA
 TTGATCATGCGCGCCGAGGGCGGGCTTTGGCTGCGGGTGGAGCCCCGAATGTAGGCTTGCA
GTGACTTCTGACCATCCACCTGTTTTTTTTCAGATTGTGCATGAATAAAACGGTGTGTCAA

FIGURE 182

MSLLSLPWLGLRPVAMSPWLLLLLVVGSWLLARILAWTYAFYNNCRRLQCFPQPKNWFWG
 HLGLITPTEEGLKDSTQMSATYSQGFTVWLGPIIPFIVLCHPDTIRSITNASAAIAPKDNLF
 IRFLKPWLGEKILLSGGDKWSRHRRLTPAFHFNILKSYITIFNKSANIMLDKWQHLASEGS
 SRLDMFEHISLMTLDSLQKCIFFSDSHCQERPSEYIATILELSALVEKRSQHILQHMDFLYY
 LSHDGRRFHRCRLVHDFTDVIRERRRTLPTQGIDDDFFKDKAKSKTLD FIDVLLLSKDEDEG
 KALSDEDIRAEADTFMFGGHDTTASGLSWVLYNLARHPEYQERCQEVQELLKDRDPKEIEW
 DDLAQLPFLTMCVKESRLRHPPAPFISRCCTQDIVLPDGRVIPKGITCLIDIIGVHHNPTVW
 PDPEVYDFFRFDPENSKGRSPLAFIPFSAGPRNCIGQAFAMAEMKVVLALMLLHFRFLPDHT
 EPRRKLELIMRAEGGLWLRVEPLNVGLQ

$\begin{pmatrix} 1 & 0 \\ 0 & 1 \end{pmatrix}$
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 $\begin{pmatrix} 0 & 0 \\ -1 & -1 \end{pmatrix}$

FIGURE 183

CAACAGAAGCCAAGAAGGAAGCCGTCCTATCTTGTGGCGATC**ATG**TATAAGCTGGCCTCCTGC
TGTTTGCTTTTCACAGGATTCTTAAATCCTCTCTTATCTCTTCCTCTCCTTGACTCCAGGGA
AATATCCTTTCAACTCTCAGCACCTCATGAAGACGCGCCTTAACTCCGGAGGAGCTAGAAA
GAGCTTCCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAGAGGGGATATTCTCAGG
AAAGCAGACTCAAGTACCAACATTTTTTAACCAAGAGGAAATTTGAGAAAGTTTCAGGATTT
CTCTGGACAAGATCCTAACATTTTACTGAGTCATCTTTTGGCCAGAATCTGGAAACCATACA
AGAAACGTGAGACTCCTGATTGCTTCTGGAAATACTGTGTC**TGA**AGTGAAATAAGCATCTGT
TAGTCAGCTCAGAAACACCCATCTTAGAATATGAAAAATAACACAATGCTTGATTGAAAC
AGTGTGGAGAAAACTAGGCAAACACACCCTGTTTCATTGTTACCTGGAAAATAAATCCTCT
ATGTTTTGCACAAAAAAAAAAAAAA

FIGURE 184

MYKLASCCLLFTGFLNPLLSLPLLDREISFQLSAPHEDARLTPEELERASLLQILPEMLGA
ERGDILRKADSSTNIFNPRGNLRKFQDFSGQDPNILLSHLLARIWKPYKKRETPDCFWKYCV

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FIGURE 185

GAACATTTTGTAGTTCCCAAGGAATGTACATCAGCCCCACGGAAGCTAGGCCACCTCTGGGAT
 GGGGTTGCTGGTTTAAACAAACGCCAGTCATCCTATATAAGGACCTGACAGCCACCAGGCA
 CCACCTCCGCCAGGAAGTGCAGGCCACCTGTCTGCAACCCAGCTGAGGCCATGCCCTCCCC
 AGGGACCGTCTGCAGCCTCCTGCTCCTCGGCATGCTCTGGCTGGACTTGGCCATGGCAGGCT
 CCAGCTTCTGAGCCCTGAACACCAGAGAGTCCAGCAGAGAAAGGAGTCGAAGAAGCCACCA
 GCCAAGCTGCAGCCCCGAGCTCTAGCAGGCTGGCTCCGCCCCGAAGATGGAGGTCAAGCAGA
 AGGGGCAGAGGATGAACTGGAAGTCCGGTTCAACGCCCCCTTTGATGTTGGAATCAAGCTGT
 CAGGGGTTCAGTACCAGCAGCACAGCCAGGCCCTGGGGAAGTTTCTTCAGGACATCCTCTGG
 GAAGAGGCCAAAGAGGCCCGCAGCCGACAAGTGATCGCCACCAAGCCTTACTACCTCTCTCT
 AAGTTTAGAAGCGCTCATCTGGCTTTTCGCTTGCTTCTGCAGCAACTCCCACGACTGTTGTA
 CAAGCTCAGGAGGCGAATAAATGTTCAAAGTGA

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FIGURE 187

CGGCCACAGCTGGCATGCTCTGCCTGATCGCCATCCTGCTGTATGTCTCGTCCAGTACCTC
 GTGAACCCCGGGTGTCCGCACGGACCCAGATGTCAAGAATATGAAACACGTGGCTGCTGT
 TCCTCCCCCTGTTCCCGGTGCAGGTGCAGACCCTGATAGTCGTGATCATCGGGATGCTCGTG
 CTCCTGCTGGACTTTCTTGCTTGGTGCACCTGGGCCAGCTGCTCATCTTCCACATCTACCT
 GAGTATGTCCCCACCCTAAGCCCCGATCCCCCAAGGCTGGTGGTCAGAGCTGCTCATC
 TTACACCTCTACTTGAGTATGTCCCTAACCTGAGCCCCCACGCCTGGGGCCAGAGTCTTT
 GTCCCCGTGTGCGCATGTGTTCAGGGTCAGCCTCTCCAGAAGTGAGATCATGGACAAAA
 GGGCAATCACAGGAAGAAATTAATCCATGAGGACCCAGCAGGCCAGCAAGAAGCTGAAC
 TCACGCCGAGACCTGCAGGAGTGGTGCCAGGTGCTTGAAGTAACAAGTTTAAATGTTTCAGA
 GACAATGGAATGGAATCTATTAGGCAAGAACAGGCATTATGAAATAAGGACAGGTGGACTT
 CCAAAAACACAAGTAGAAATTCTAACAATGAAATATATTACAGGCAGGTCACCCCTAACCA
 AACAACTGAAGCGAGAGCTGTGGTCTTGCTTGGTCTCACAGTGGGCACAGCGGTAGGCGGTC
 AGTCATGTTGCTGAACGACGGAGGGTAAACTCCCCAGCCCCAAGAAAACCTGTGTTGGAAGT
 AACAAACACCTCCCTGCTCCTGGCACCAGCCGTTTTGGTCATGGTGGGCCAGCTGCAAAGCG
 TCTTCCATTCTCTGGGCAGTGGTGGCCCCGAGGCTGTGGCCTCTCAGGGGTTTCTGTGGAC
 ACGGGCAGCAGAGTGTGTCCAGGCCAGCCCCAAGAATGCCCTGCTCCTGACAGCTTGGCCA
 ACCCTTGGTCAGGGCAGAGGGAGTTGGGTGGGTGAGGCTCTGGGCTCACCTCCATCTCCAGA
 GCATCCCCCTGCCTGCAGTTGTGGCAAGAACGCCAGCTCAGAATGAACACACCCCCACCAAGA
 GCCTCCTTGTTCATAACCACAGGTTACCTACAAACCACTGTCCCCACACAACCTGGGGAT
 GTTTTAAACACACACCTCTAACGCATATCTTACAGTCACTGTTGTCTTGCTGAGGGTTGA
 ATTTTTTTTAATGAAAGTGAATGAAATCACTGGATTAAATCCTACGGACACAGAGCTGAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

188/330

FIGURE 188

MNTWLLFLPLFPVQVQTLIVVIGMLVLLDLFLGLVHLGQLLI FHIYLSMSPTLSPRSPQGW
VVRAAHLTPLLEYVPNPEPPTPGARVFVPRVRMCSGSASPRSEIMDKKGSQEIKSMRTQQ
AQQEAELTPRPAGVVPGA

188/330

FIGURE 189

GGAGTGCAGATGGCATCCTTCGGTTCTTCCAGACAAGCTGCAAGACGCTGACCATGGCCAAAG
 ATGGAGCTCTCGAAGGCCTTCTCTGGCCAGCGGACACTCCTATCTGCCATCCTCAGCATGCT
 ATCACTCAGCTTCTCCACAACATCCCTGCTCAGCAACTACTGGTTTGTGGGCACACAGAAGG
 TGCCCAAGCCCCCTGTGCGAGAAAGGCTCGGCAGCCCAAGTGCTTTGACATGCCAGTGTCCCTG
 GATGGAGATACCAACACATCCACCCAGGAGGTGGTACAATACAACCTGGGAGACTGGGGATGA
 CCGGTTCTCCTTCCGGAGCTTCCGGAGTGGCATGTGGCTATCCTGTGAGGAAACTGTGGAAG
 AACAGGGGGAGAGGTGCCGAAGTTTCATTGAACCTTACACCACCAGCCAAGAGAGGTGAGAAA
 GGACTACTGGAATTTGCCACGTTGCAAGGCCCATGTACCCCACTCTCCGATTTGGAGGGAA
 GCGGTTGATGGAGAAGGCTTCCCTCCCTCCCTCCCTTGGGGCTTTGTGGCAAAAATCCTA
 TGGTTATCCCTGGGAACGCAGATCACCTACATCGGACTTCAATTCATCAGCTTCTCTCTGCT
 ACTAACAGACTTGCTACTCACTGGGAACCCTGCCTGTGGGCTCAAACCTGAGCGCCTTTGCTG
 CTGTTTCTCTGTCTGTCTGAGGTCTCCTGGGGATGGTGGCCACATGATGTATTACAAGTC
 TTCCAAGCGACTGTCAACTGGGTCCAGAAGACTGGAGACCACATGTTTGGAAATTATGGCTG
 GGCCTTCTACATGGCCTGGCTCTCCTTCACTGCTGCATGGCGCTCGGCTGTACCACCTTCA
 ACAGTACACCAGGATGGTGCTGGAGTTCAAGTGCAAGCATAGTAAGAGCTTCAAGGAAAAAC
 CCGAAGTGCCTACCACATCACCATCAGTGTTCCTCGGGGGCTGTCAAGTGCAGCCCCCAG
 CGTGGGTCCTTTGACCAGCTACCACCAGTATCATAATCAGCCCATCCACTCTGTCTCTGAGG
 GAGTCGACTTCTACTCCGAGCTGCGGAACAAGGGATTTCAAAGAGGGGCCAGCCAGGAGCTG
 AAAGAAGCAGTTAGGTCATCTGTAGAGGAAGAGCAGTGTTAGGAGTTAAGCGGTTTGGGGA
 GTAGGCTTGAGCCCTACCTTACACGTCTGCTGATTATCAACATGTGCTTAAGCCAACATCCG
 TCTCTTGAGCATGGTTTTTTAGAGGCTACGAATAAGGCTATGAATAAGGGTTATCTTTAAGTC
 CTAAGGGATTCTGGGTGCCACTGCTCTCTTTTCTCTACAGCTCCATCTGTGTTTCAACCCAC
 CCCACATCTCACACATCCAGAATTCCCTTCTTTACTGATAGTTTCTGTGCCAGGTTCTGGGC
 TAAACCATGGAGATAAAAAGAAGAGTAAAATACACTTCCCGACCTTAAGGATCTGAAA

FIGURE 190

MAKMELSKAFSGQRTLLSAILSMLSLSFSTTSLLSNYWFVGTQKVPKPLCEKGLAAKCFDMP
VSLDGDNTNTSTQEVVQYNWETGDDRFSEFRSFRSGMWLSCEETVEEPGERCRSFIELTPPAKR
GEKGLLEFATLQGPCHPTLRFGGKRLMEKASLPSPPLGLCGKNPMVIPGNADHLHRTSIHQL
PPATNRLATHWEPCLWAQTERLCCCFLCPVRSPGDGGPHDVFTSLPSDCQLGSRRLETTCL
LWLGLLHGLALLHLLHGVGCHHLQHVVHQDGAGVQVQA

190/330

FIGURE 191

AACTGGAAGGAAAGAAAGAAAGGTCAGCTTTGGCCCA**ATG**TGGTTACCCCTTGGTCTCCTG
 TCTTTATGTCTTTCTCCTCTTCTATTTCTGTCATCTCCCTCACTTAAGTCTCAGGCCTGTCA
 GCAGCTCCTGTGGACATTGCCATCCCCCTCTGGTAGCCTTCAGAGCAAACAGGACAACCTATG
 TTATGGATGTTTCCACCAACCAGGGTAGTGGCATGGAGCACCGTAACCATCTGTGCTTCTGT
 GATCTCTATGACAGAGCCACTTCTCCACCTCTGAAATGTTCCCTGCTCTGAAATCTGGCATG
 AGATGGCACAGGTGACCACGCAGAAGCCACCAGAATCTTGCCTGCCCTATTCTCCTCCCAA
 GTCTGTTCTCTTATTGTCAACCTCAGCACAAACAGGCTGGCGCCAATGGCATTACAGAGAAAG
 CAATCTGTGTGGCTAGTGGGCAGATTACCATGCAAGCCCCAGGAGAAATGGAGGAGCTTTGT
 AGCCACCTCCCTGTGAGCCAGTATTAACATGTCCCCTTCCCCCTGCCCGCCGTAGATTGAG
 GACATTCGCCCTGTGTGCCACCAACCAGGACTTCCCCTTGGCTTGGCATCCCTGGCTCT
 CTCTGTTACCCAGCAAGACGTCTGTTCCAGGGCAGTGTAGCATCTTCAAGCTCCGTTACT
 ATGGCGATGGCCATGATGTTACAATCCCACTTGCCTGAATAATCAAGTGGGAAGGGGAAGCA
 GAGGGAATGGGGCCATGTGAATGCAGCTGCTCTGTTCTCCCTACCTGAGGAAAAACCAA
 GGGGAAGCAACAGGAACTTCTGCAACTGGTTTTTATCGGAAAGATCATCCTGCCCTGCAGATGC
 TGTGGAAGGGGCACAAGAAATGTAGCTGGAGAAGATTGATGAAAGTGCAGGTGTGTAAGGAA
 ATAGAACAGCTGCTGGGAGTCAGACCTGGAATTTCTGATTCCAACTCTTTATTACTTTGGG
 AAGTCACTCAGCCTCCCCGTAGCCATCTCCAGGGTGACGGAACCCAGTGTATTACCTGCTGG
 AACCAAGGAACTAACAATGTAGGTTACTAGTGAATACCCCAATGGTTTCTCCAATTATGCC
 CATGCCACCAAAACAATAAAACAAATTCTCTAACACTGAAA

FIGURE 192

MWLPLGLLSLCLSPILSSPSLKSQLQACQQLLWTLPSPLVAFRANRTTYVMDVSTNQSGME
HRNHLCFCDLYDRATSPPLKCSLL

192/330

FIGURE 193

GTAGCGCGTCTTGGGTCTCCCGGCTGCCGCTGCTGCCGCCGCCGCTCGGGTCGTGGAGCCAGGAGCGACGTCA
 CCGCCATGGCAGGCATCAAGCTTTGATTAGTTTGTCTCTTTGGAGGAGCAATCGGACTGATGTTTTTGTATGCTT
 GGATGTGCCCTTCCCAATATACACAAATACTGCCCTCTTTGTCTCTATTTTATACATCCCTTCACTTATCC
 ATACTGCATAGCAAGAAGATTAGTGGATGATACAGATGCTATGAGTAACGCTTGAAGAACTTGCCACTCTTTC
 TTACAAAGGGCATTGCTGTGCAGCTTTTGGACTCCCTATTGTATTTGCCAGAGCACTCTGATTGAGTGGGA
 GCTTTGTCACCTTGTCTCACAGGAAACACAGTCACTCTTTCCAACTATACCTAGGCTTTTCTTGCTCTTTGGAAG
 CTAATGACGACTTCACTGGCAGCAGTGGCTGAAGAAATTAAGTAATTTGTCAAAATGGACTTCTCTGCACTT
 GTTGCCCATTCACGCACACAGGAGATGGGGCAGTTAATGCTGAATGGTATAGCAAGCCCTCTGGGGGTATTTTA
 GGTGCTCCCTCTCACTTTTATTGAAGCATACTATTTTACAGAGACTTGTCTGAAGGATTAAGAGGATTTTCI
 CTTTTGAAAAGCTTGACTGATTTTCACTTATCTATAGTATGCTTTTGTGGTGTCTGCTGAATTTAAATAT
 TTTATGTGTTTTCTGTTAGGTTGATTTTTTTTGGAAATCAATATGCAATGTTAAACACTTTTTTAAATGTAATCA
 TTTGCATTGGTTAGGAATTCAGAATTCGCCGGCTCTATTACTGGTCAAGTACATCTTTCTCTTAAATTTAT
 TAGCCTCCATTATACAAAAAATATAAAAAAAGTTTTCACTGAGTCAGGATGACATCACTCCCAATGTTATG
 CAGACATACAGACGGTTGGCATACTTATAGACTGTATACTCAGTGCAAAATATAGCTGCATTTATACCTCAGAG
 GGGCCAAAGTGTAAATGCCATGCCCTCCGTTAAGGGTTGTTGGTTTTACTGGTAGACAGATGTTTTGTGGATTG
 AAAATTATTTTATGGAATGCTACAGAGGAGTGCTTTTCTCTCAATTGTTAAGAATTTATGTTAAACCTTA
 AGGTAAGGGTGTAAGAACTTTTGGAGATAAGGTTTTTATTATGTTTATTATTGTTAGAGTGAGTTGCAATGT
 GGGGAAGAAATGACATTGAATTCAGTTTTTGAATCCTGTTTCTATTATAAGTGAAATTTGTGATCTCCTATC
 AACCTTTCATGTTTTACCTCTGTTAAATGGACATACATGGAACCACTACTGATGAGGGACAGTTGATGTTTGC
 ATCATATATGCCAGAAAACCTTCTCTGCTTCTCCTTTGACTTATTTGGTATGTTGTATATATTACATAAAA
 TAACTTTTCAATATAGTTTAAATAACACTTAGAAGTGTTAACCTACCTGGAAAAATAAATGCTATGCCGTACATT
 CAGAGTGCCCTCCCTGCAAGGCCCTGCCATGATTAAACAAGTAACTTTAGTCTACAGATAATTCATGCA
 TATTTTAAGACAGTTTTCTGTATACCTCTGAAGTGTGTTGATTTGAGTTCATCATGATAGATCTGCTGTTT
 CCTTATAAAGGCAATTTGTGTGAGTTAATGCAAGTAGCCAAGTCCAGCTATATAGCAGCTTCAGAAACAT
 ACCTGACCAAAAAATTTCCAGTAACAGGCATGATCAATTTATAGTGGTCGTTTACATCTAATAATTATCAGGA
 CTTTTTTCAGGAGTGGGTATAAAAAACATTCAAGTTGGTCTGACAGTATTTTGTGAAGGATATTTGTTGTATG
 TTTATTCAGTATACCTACATAAAAAATTTTCGCCATCAGCCAAAACCTCAGTAATCATGACAGCTGTCTGTGTT
 TTTATGAAGTTTATTTCTCAAGAAATGGGAATAAATTTGGGATTTGTTCAAGCTTTTACTTAAAGATGCCTAA
 AGCCACAGGTTTTATTGGCCTAACTTAAGCCATGACTTTTAGATATGAGATGACGGGAAGCAGGACGAATATCG
 CGCTGTGGCTGGACCTTCCCACTGGAGGCTGAAAGTGGCTTGTGGTATTAATGTTCAAGATTTCAAGAGGAA
 GGTGCAGGTACACATGAGTTAGAGAGTGGTGAGACAGTTGGGAACCTTTGTGCTGTGATCTACTGACCTTT
 TTTTTCAGGAAGTGCATTTCTGCTGCTTCCCTATTTCTGTTCTGGATGTCAGTGCAGTGCAGTGCCTACTG
 TTTTATCACTTGGCCACAGACTTTTCTAACAGCTGCGTATTTCTATATACATATGCAATTTGCAATGGCAGCTT
 GTGTCTTTGACCTTGTATACCTAGCTTGACATACCTGCTGCTCTGATTTCAGGCTAGTTACTTGAGATATGAAT
 TTTCCATAGATATGCACTGATACCAATACCATTCTTCTATGGAAGAAAACCTTTTGATGATGAACAATAA
 AGATTTTAAATCTATTTTAAAAA

FIGURE 194

MAGIKALISLSFGGAIGLMFLMLGICALPIYNKYWPLFVLFFYILSPIPYCIARRLVDDTDAM
SNACKELAIFLTGTGIVVSAFGLPIVFARAHLEWGACALVLTGNTVIFATILGFFLVFGSND
DFSWQQW



CAACGGCTCGCCGCAACCTCGCCGCCACGCTCCGCGACGGCTCGCCGCAACGGCTCGCCGACGGCTCGCGG
CAGCGCTCCGGTGCAAGCTCGGCCGCGACAGCTGCTGGTGAGGGGAAGGAGCCGGGGCGCTCTCGCGCTCGG
CGCGCGAGCTGCTCGACACTCTCCACCGCCGCGCGGCCCGCCGCGCCGCGCCGCAAGAAGATGAGTGCACCGCTC
CTGCGACGCTCGCCGGGGCGCAATGGCAGCTGTTTCCGCGAGATGAAAAGTGGCGCGGTCAGTGGTGCTTTC
CAATGACGGAACATGAACCCAGATCTGCAGATCTCGGGGATTCGCGAGGCCGCGAGTTTGGAGTTTTCCTCCCG
AAGTGCACAGTCCGAATCGCAGAGGAAGAAGCGCGAGGAAGCGAGAGCTCGGGCGAGCGATCTGATGGT
GAAATCTGCGGGTCTGATGAAGTCTGCGCGCGCGCGCGACGGGGTCTCTCGGAACACAGAGGGGTCTTCTCTC
GCCCTGCATATAATAGCTCTGCACACAAAGGAGGACGCTGAATGAGGATGTGTACTCTCGAAAGAAATTTCT
GACCGAGCGCTTCAATGACATCTTCCAGTCTCTGGAAGAATTTCTCGCTAATGATTTCTGCTGCTCGCT
CTCTGCTACTTGGCTGTGAGGAGGCCCTCGGGGGGCTCTGTGTCTGCTGGGGGGCTCTTTAGATGCT
TCCCGCGCCCGCCCGAGCGGGTGGCCGCGACTGTGCGGCTGCGAGGGGGCGGTGTGTACTGCGAGGCGCTCAAC
TACCGAGAGCGCCCCAACCTCTGCGGCGTCTGGGCTGTGCTCGGTCGACACAGAGCTCTCGAGAGCTCGC
CGCGCGCAGTCTCCAGCGGTTAATGACCTACGCTGGCTCTATCTGGATCAGATCTGAGATGATGATGATG
GAGTGGCGCTGATGATGAGTGTGCTGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG
CAACTTCTCGGCCCATCCCAACGCGCGACGCTGGACCTTCGTGACAAACAGATCAGGCGCTCGGCCAAC
CTTCTCCAGCGGCTCGGAGAGCTCACCGACCTGATATCGGGGCAACGCCATCAAGTTTGTGCGGCTGCGGAT
CTTTCAGGAGTCCGCGAGCTCAAGTTTCTGCAGATCGATACATCAGTCAAGAGTCTGGCGCGCAACTTCT
TGCGGCGGTTGTTTAAGCTCACCGAGTCTGCACTCTGAGCACACAGCACTTGGTCAAGGTGAATTCGCGCACTT
CGCGGCTCATCTCCCTGCACTGCTTGCCTCGCGAGGAAACAGTGGCCATCTGTGGTCACTCTCGGAGTGT
GGTTGAGTCTGATGAGAAATGAGTCTGCG
GCGCGCGCTGATGATGAGTGTGCTGCGCGCGCTCACCTACGATCAGGCTCGGATCGATGATGATGATGATG
AAGTCCCTCAACAGCATCACCTCGCGGGAGAGTGTGGATTCGCGGCGCAAGCTGTGTGCCCTGAGCTGTG
GCTCAACAACTTCAGGGGCGTACGATGAGCACTTCAGTGGCGCGAGCCCGGAGTACGACACAGGCGAGGAGC
TCTGCGAGCGCGTGTAGCGCTTCCACTGTGCGAGAGATGGGCGCGAGCCACAGCGCGGCACTGCTCTCGGC
TGCAACAAACCGCAGTGTCTGGGGCGCCCTCGCAGCTCGGCGCACACAGCTCTCGCGAGACCGGGGAGGGCAG
CGACGCGCATCTGAGCTGCGACCTGGCTGCG
AGGTTGCTGCTGATGAGTGTGCTGCTGCT
GCTG
CTGATCTCAGAGTGGCTGCGATGTCTGCTCGCCAGGAATACGTTGTATTACAAACGAACCACTTGAAGGAG
TGGTGTGATCTCAACGAGTAGTGTGCTGTGATCTGCCACAGAGCCGCGAGGGAATGCGAGGTTCTGATTGCT
CGATGCTCTCAACCAATCGCTCAACAAATGCTGGCGAGCGGGAGCGCGCGGCGCGGCGCGAGCTGGGTT
CTCCTGTGCTGCTGCTGCTGATGTGCTCTTGACTGAAACTTTAAGGGGCTCTCTCCCGAGACTTGACATTTAG
TTTTTGTGTGCTTTAAACAAAGAGCTTAATTAACATGAATAAAACATGATGATGATGATGATGATGATGAT
TTCTGCT
AAAGGTGGCTATAGACAGAGAGAATAATCTGCTGTTTGTATGCTACTCTCCACCTGCCCATGGATTA
AACTCATGTGTTCTAGAGATCTTAAGTCTATCGATTCTCATGAGAACATTTGAAAGAGGAATCTGCAAT
TGGGAGCTTAAGAGCAATGATGACATAGAAGACTGTTTCTTACTGTTGTGTGTGTGTGTGTGTGTGTGT
TTGTGTGCTCTGTAGGCAAGAAAGCTGTGCTACACAACCGGGAATTTAGTGCATCATCTTCTGCCCTGT
GCGCTGATCTGTGAGATGTGGGGGGAGGTGGGGGAGAACGCGAGGAATAGGGAAGAGTGTGATGATGAT
AGCGCTG
CTCTAAGCAACTACTAAGACTTTAAAGAGACTTAATTTTAAAGGTGTAGCACTTTTTTTATCTTCC
CCACAGAGGGTGCTAATCTCATTTGCTGTCTATCTGAAAGAACTTAAGGCGCAAAATCACGTTCTCGCT
GGCATTTGTATGGATTGACCTTCAATTTGCGATCACTTCCAGCTGATTAAAGTTCAGAGTGTGATTGAGTT
TTTTCGAATTTTATATAGAAAGAAAGTTTTCATGTACAAATGACACTCTCACACAGCTCTTAGGCTAGTA
GTTTTTATGTTTGGACAGGAGAGCAGTTTAATGACATCTCTCTGCTGCACTCAGAAAATAAGGCACTCT
CTGATGCTCTGAT
GAT
TCTCTGAACTCATCAAGTAGAAGAGGCCCAACTTTTCTCTCGCTCTAAGAGAGGACAGATTTGGTAT
ATTTAGCATCAACACACATTTATGATGATATGTAGTATGACAGAGGGCAATGCCATCTGTTATTTCTCCA
AGTTTTCGAAGCAAGTACACAGATCTCTGATGAGATTAGGGCGCACTGTGTTTTCGGGTTTATTTATGTC
CTGTGACGAAGTTTGTATGCTGATCTATCTGACATGCGCCGATGAGACAGGGCATTTGATGATGATGATGAT
GGTAGAAGAACATCTCAGTCTCAGTCTCTCAGCAGAAATTTAGAGACAGAAATTTAGAGAGAGAGAGAG
GAT
CTGATTTGGCTTCCGATTCGACATGACAGATTCGAATTAAGAAATAGTCTAGATATGACCATTAATTTGTCTT
CTGAATATATTTTGAAGAGTTTGTAGATGTCTCA

FIGURE 196

MDFLLGLCLYWLLRRPSGVVLCLLGACFQMLPAAPSGCPQLCRCEGRLLYCEALNLTEAPH
NLSGLLGLSLRYNSLSELRAQFTGLMQLTWLYLDHNHICSVQGDADFQKLRRVKELTLSSNQ
ITQLPNTTFRMPNLRSDLSYNKLQALAPDLFHGLRKLTLHMRANAIQFVPVRI FQDCRS
LKFLDIGYNQLKSLARNSFAGLFKLTEHLHENDLVKVNFAHFPRLISLHSLCLRNRNKVAIV
VSSLDWVWNLEKMDLSGNEIEYMEPHVFETVPHLQSLQLDSNRPTYIEPRILNSWKSLSIT
LAGNLWDCGRNVCALASWLSNFQGRYDGNLQCASPEYAQGEDVLDVAVYAFHLCEDGAEP TSG
HLLSAVTNRSDLGPPASSATTLADGGEGQHDGT FEPATVALPGGEHAENAVQIHKVVTGTMA
LIFSFLIVVLVLYVSWKCFPASLRQLRQCFVTQRRKQKQKQTMHQAAMSAQEY YVDYKPNH
IEGALV IINEYGSCTCHQQPARECEV

FIGURE 197

GTGCAAGGAGCCGAGGCGAG**ATG**GGCGTCCTGGGCCGGGTCCTGCTGTGGCTGCAGCTCTGC
GCACTGACCCAGGCGGTCTCCAAACTCTGGGTCCCCAACACGGACTTCGACGTCGCAGCCAA
CTGGAGCCAGAACCGGACCCCGTGCGCCGGCGGCCGTTGAGTTCGCCGCGGACAAGATGG
TGTCAGTCCTGGTGCAAGAAGGTACGCCGTCTCAGACATGCTCCTGCCGCTGGATGGGGAA
CTCGTCCTGGCTTCAGGAGCCGGATTCCGGCGTCTCAGACGTGGGCTCGCACCTGGACTGTGG
CGCGGGCGAACCTGCCGTCTTCCGCGACTCTGACCGCTTCTCCTGGCATGACCCGCACCTGT
GGCGCTCTGGGGACGAGGCACCTGGCCTCTTCTTCGTGGACGCCGAGCGCGTGCCCTGCCGC
CACGACGACGTCTTCTTCCGCCTAGTGCCTCCTTCCGCGTGGGGCTCGGCCCTGGCGCTAG
CCCCGTGCGTGTCCGCAGCATCTCGGCTCTGGGCCGGACGTTACGCGCGACGAGGACCTGG
CTGTTTTCTGCGCTCCCGCGGGGCCGCTACGCTTCCACGGGCCGGCGCGCT**TGA**GCGTG
GGCCCCGAGGACTGCGCGGACCCGTCCGGGCTGCGTCTGCGGCAACGCGGAGGCGCAGCCGTG
GATCTGCGCGGCCCTGCTCCAGCCCCT

198/330

FIGURE 198

MGVLGRVLLWLQLCALTQAVSKLWVPNTDFDVAANWSQNRTPCAGGAVEFPADKMVSVLVQE
GHAVSDMLLPDGLVLASGAGFGVSDVGSHLDCGAGEPAVFRSDRFSWHDPHLWRSGDEA
PGLFFVDAERVPCRHDDVFFPPSASFRVGLGPGASPVVRVRSISALGRFTTRDEDLAVFLASR
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FIGURE 200

MGPVKQLKRMFEPTRLIATIMVLLCFALTLCSAFWWHNKGALIFCILQSLALTWYSLSFIP
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FIGURE 201

TTGAGCGCAGGTGAGCTCTCGCGCTTCGGGGGGCGTTCCTCCAGTCACCCCTCCGCGGTTACCGCGCGCGCGC
 CCGAGGGAGTCTCTCCAGACCCCTCCCTCCCGTTGCTCCAACTAATACGGACTGAACGGATCGCTCGCAGGGI
 GGGAGAGAAAATAGGGGGAGAAAGGACAGAGAGGCACTACCATCCATAGCCAGATAGATTATCTTACACTG
 AACTGATCAAGTACTTTGAAAATGACTTTCGAAATTTATCTTGGTGCTTTCATCTTGGTGCATGAGTCTTTC
 AACCACTTTCTCTCCCACTAGACAGCAAAAGGTTCTACTAGTTCTTTTGGATGGATTCCGTTGGGATTACT
 TATATAAGGTTCCAAACGCCCATTTTCATATATATATGAATATGGTGTACAGTGAAGCAAGTTACTAATGTT
 TTTATACAAAACCTACCCATAACCATATATCTTTGGTAAGTGGCCTCTTGCAAGAGAAATCATGGGATTGTTGC
 AAATGATATGTTTGGTCTATTCGGAACAAATCTTCTCCTTGGATCACATGAATATTTATGATTTCAAAGTTT
 GGGAGAGAGCAGCAACCAATATGGATCACAAACAGAGGGCAGGACATACTAGTGGTGCAGCCATGTGGCCCGGA
 ACAGATGTAAAAATACATAAGCGCTTTCCCTACTCATACATGCCTTCAATGAGTCAGTTTCATTTGAAGATAG
 AGTTGCCAAATTTGTTGAATGGTTTACGTCAAAGAGCCCAATAATCTTGGTCTTCTCTATTGGGAAGACCCCTG
 ATGACATGGGCCACCATTTGGGACCTGACAGTCCGCTCATGGGGCTGTCAATTTGAGATATTGACAAAGAGTTA
 GGATATCTCATACAAATGCTGAAAAGGCAAGTTTGGGAACACTCTGAACCTAATCATCACAGATGATCATGG
 AATGACGCGAGTCTCTGAGGAAAGGTTAATAGAACTTGACCAGTACCTGGATAAGACCATATACCCTGATTG
 ATCAATCTCCAGTAGCAGCCATCTTGC AAAAGAGGTAATTTGATGAAGTCTATGAAGCACTAACTCACGCT
 CATCCTAATCTTACTGTTTACAAAAAGAGACGTTCCAGAAAGGTGGCATTTACAAATACAACAGTCGAATTC
 ACCAATCATAGCAGTGCTGATGAAGGTTGGCACATTTACAGAAATAGTCAGATGACTTTCTGTTAGGCAACC
 ACGGTTACGATAATGCTGTAGCAGATATGCATCCAATATTTTAGCCCATGGTCTGCTTCAGAAAAGAAATTC
 TCAAAAGAGCCATGAATCCACAGATTTGTACCACTACTATGCCACCTCCTCAATATCACTGCCATGCCACA
 CAATGGATCATCTGGAATGTCAGGATCTGCTCAATTCAGCAATGCCAAGGTTGGTCCCTTATACACAGATTA
 CTATACTCTCCCTGGTATGTTAAACAGCAGAAATATGACCAAGAGGGGTCTATCCCTTATTTATAGGGGTCT
 TCTCTTGGCAGCATTATAGTGATGTTATTTTGTATTTTTCATTAAGCATTTAATTCACAGTCAAATACCTGC
 CTTCACAGATATGCATGCTGAATAGCTCAACCATTTATACAAGCCTAATGTTACTTTGAAGTGGATTTGCATA
 TTGAAGTGGAGATTCCTCAATATATGTCAGTGTTTAAAGGTTTCAAATTTCTGGAAACAGTTTCCAAACATCTGC
 AGAAACCATTAAGCAGTACATATTTAGGTATACACACACACACACACATACACACACAGGACCAAA
 ATACTTACACCTGCAAGGATAAAGATGTGAGAGTATGCTCCATTTTCACTGTAGCATAGGGATAGATAAG
 ATCCTGCTTTATTTGGACTTGGCGCAGATATGTATATTTAGCACTTTGCACTATGTAAGTACCTTATAT
 ATTGCATTTAAATTTCTCCTGATGGGTACTTTAAATTTGAATGCATTTATGGACAGTTATGCTTTATAAC
 TTGATGAAAATGACACTTTTGCACCCATGTACAGAAATCTTGTACGCATTTGTTCAAACGAGGAAAT
 TCTAATAATCCCGAATAATGAACATAGAAATCTATCTCCATAAATGAGAGAAGAAGGATGATAAGTGTGA
 AAATTAATGTTGATAACCTTTGAACCTTGAATTTTGGAGATGATTTCCCAACAGCAGAAATGCACTGTGGCAT
 TTTCTTGTCTTATTTCTTCCAGAGAAGCTGGTTTCATTTATTTTCCCTCAAAGAGAGTCAAATACAGACAG
 ATTCGTTCTAATAATATTTGTTTCTGTCATAAAATATTGTGATTTCTGATGAGTCATATCTGATGTTTCTCA
 TAATAATGAAGACCACTAGATAATACITTTCTCTATATAGTTACCAATGGCTCAATAGAAGCAACAGGCA
 CCATCTCAGCAATGTTTCTCTTGTGTAATATTTGCTCCTTTGAAAATTAATCACTATTAATACATTAA
 AAATCAAAATGGATAAAAAAAAAAAAAAAAAA

FIGURE 202

MTSKFILVSFILAALSSTTFSLSQLDQQKVLVSFDGFRWDYLYKVPTPHFHYIMKYGVHVK
 QVTNVFITKTYPNHYTLVTGLFAENHGIVANDMFDPIRNKSFSLDHMNIYDSKFWEETPIW
 ITNQRIGHTSGAAMWPGTDVKIHKRFPTHYMPYNESVSFEDRVAKIVEWFTSKEPINLGLLY
 WEDPDDMGHHLGPDSPLMGPVISDIDKKLGYLIQMLKKAKLWNTLNLIITSDHGMTQCSEER
 LIELDQYLDKDHYTELIDQSPVAAILPKEGKFDEVYEALTHAHPNLTVYKKEDVPERWHYKYN
 SRIQPIIAVADEGWHILQNKSDDFLLGNHGYDNALADMHPIFLAHGPAFRKNFSKEAMNSTD
 LYPILLCHLLNITAMPHNGSFWNVQDLLNSAMPRVVPYTQSTILLPGSVKPAEYDQEGSYPYF
 IGVSLGSIIVFFVIFIKHLIHSQIPALQDMHAEIAQPLLQA

Signal Peptide:

amino acids 1-22

Transmembrane Domain:

amino acids 429-452

N-glycosylation sites:

amino acids 101-104, 158-161, 292-295, 329-332, 362-365, 369-372, 382-385, 389-392

Somatomedin B Domain:

amino acids 69-85

Sulfatase protein Region:

amino acids 212-241

FIGURE 203

GGATTTTGTGATCCGCGATTTCGCTCCACGGGCGGGACCTTTGTAACTGCGGGAGGCCAG
 GACAGGCCACCCCTCGGGGCGGGAGGCAGCCGGGTGAGGAGGTGAAGAAACCAAGACGC
 AGAGAGGCCAAGCCCTTGCCCTGGGTACACAGCCAAAGGAGGCAGAGCCAGAACTCACAA
 CCAGATCCAGAGGCCAACAGGGACATGGCCACCTGGGACGAAAAGGCAGTCACCCGACGGGCC
 AAGGTGGCTCCCGCTGAGAGGATGAGCAAGTTCCTTAAGGCACTTCACGGTCGTGGGAGACGA
 CTACCATGCTCGGAACATCAACTACAAGAAATGGGAGAATGAAGAGGAGGAGGAGGAGG
 AGCAGCCACCACCCACACCAGTCTCAGGCGAGGAAGGCAGAGCTGCAGCCCCTGACGTTGCC
 CCTGCCCTGGCCCCGACCCAGGGCCCCCTTGACTTCAGGGGCATGTTGAGGAACTGTT
 CAGCTCCACAGGTTTCAGGTCATCATCATCTGCTTGGTGGTTCGGATGCCCTCCTGGTGC
 TTGCTGAGCTCATCTGGACCTGAAGATCATCCAGCCCGACAAGAATAACTATGCTGCCATG
 GTATTCACACTACATGAGCATCACCATCTTGGTCTTTTTATGATGGAGATCATCTTTAATT
 ATTTGTCTCCGCCTGAGTCTTTTACCACAAGTTGAGATCCTGGATGCCCGTCGTGGTGG
 TGGTCTCATTATCCTGGACATTGTCTCCTGTTCCAGGAGCACCAGTTTGAGGCTCTGGGC
 CTGCTGATTCTGCTCCGGCTGTGGCGGTTGCCCGGATCATCAATGGGATTATCATCTCAGT
 TAAGACACGTTTCAGAACGGCAACTCTTAAGGTTAAACAGATGAATGTACAATTGGCCGCCA
 AGATTCACACCTTGAGTTCAGCTGCTCTGAGAAGCCCTGGACTGATGAGTTTGCTGTATC
 AACCTGTAAGGAGAAGCTCTCTCCGGATGGCTATGGGAATGAAAGAATCCGACTTCTACTCT
 CACACAGCCACCGTGAAAGTCTTGAGTAAATGTGCTGTGTACAGAAGAGAGAGAAGGAAG
 CAGGCTGGCATGTTCACTGGGCTGGTGTACGACAGAGAACCTGACAGTCACTGGCCAGTTA
 TCACTTCAGATTACAATCACACAGAGCATCTGCCTGTTTTCAATCACAAGAGAACAAAACC
 AAAATCTATAAGATATTCTGAAAATATGACAGAATTTGACAAATAAAAGCATAAACGTGTA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 204

MATWDEKAVTRRAKVAPAERMSKFLRHFTVVGGDDYHAWNINYKKWENEEEEEEQPPPTPV
SGEEGRAAAPDVAPAPGPAPRAPLDFRGMLRKLFSHRFQVIIICLVVLDALLVLAELILD
KIIQPDKNNYAAMVFHYMSITILVFFMMEIIFKLFVFRLSSTSLRSWMPVVVVVSFILD
VLLFQEHQFEALGLLILLRLWRVARIINGIIISVKTRSERQLRLKQMNVLAAKIQHLEFS
CSEKPLD

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FIGURE 205

CGGCTCGAGCTCGAGCCGAATCGGCTCGAGGGGCAGTGGAGCACCACGAGGCCGCCAATAT
 GCTCTGTCTGTGCTGTAGCTGCCGGTTCATCGGGGAAGCCACAGCCAGTTCAGTACTTTG
 AGTCAAAGGGGGTCCCTGCCGAGCTGAAGTCCATTTTCAAGCTCAGTGTCTTCACTCCCTCC
 CAGGAATCTCCACCTACCGCAGTGGAAAGCAGAAAAATGTACAAAGCTGGAGATAAGGACCT
 TGATGGGCAGCTAGACTTTGAAGAATTTGTCCATTATCTCCAGATCATGAGAAGAAGCTGA
 GGTGTGTGTTAAGATTTTGGACAAAAAGAATGATGGACGCTTGAAGCGCAGAGATCATG
 CAGTCCCTGCCGGGACTTGGGAGTCAAGATATCTGAACAGCAGGCAGAAAAAATCTCAGAG
 CATGGATAAAAAACGGACCATGACCATCGACTGGAAACGAGTGGAGAGACTACGACCTCTCC
 ACCCGGTGGAANAACATCCCGAGATCATCCTCTACTGGAAGCATTCACGATCTTTGATGTG
 GGTGAGAATCTAACGGTCCCGGATGAGTTCACAGTGGAGGAGAGGCCAGCGGGATGTGTG
 GAGACACCTGGTGGCAGGAGGTGGGGCAGGGGCGTATCCAGAACCTGCACGCGCCCCGTGG
 ACAGGCTCAAGGTGCTCATGCAAGTCCATGCTCCCGCAGCAACATAGGSCATCGTTGTGT
 GGTTCACCTCAGATGATTCGAGAAGGAGGGGCCAGGTCACTCTGGCGGGCAATGCCATCAA
 CGTCTCAAATTTGCCCCCGAATCAGCCATCAAATTCATGGCCTATGAGCAGATCAAGCGCC
 TTGTTGTGTAGTGACAGGAGACTCTGAGGATTCAGCAGAGGCTTGTGCGCAGGCTCTTGCA
 GGGGCCATCGCCACAGCAGCATCTACCCAATGGAGGTCTGAAGACCCGGATGGCGCTGGC
 GAAGCAGAGGCCAGTACTCAGGAATGCTGGACTCGCCAGGAGGATCTGGCCAGAGAGGGGG
 TGGCGGCTTCTACAAAGGCTATGTCCCAACATGCTGGGCATCATCCCTATGCCGGCATC
 GACCTTCGAGCTACAGAGCGCTCAAGAAATGCTGGCTGCAGCATCTGACGTGAAGACGCC
 GGACCCGAGCTGTGTTGTGCTCTGGCTGTGGCCAGTGTGCTGACCTCTGTGGCCAGTGTG
 CCGACTACCCCTGGCCCTTGTGTCAGGACCCGGATGCAAGCCCTCTATTGAGGGCGCT
 CCGGAGGTGACCATGACGACGCTCTTCAAACATATCTCGCGACCCGAGGGGGGCTTCGGGCT
 GTACAGGGGGCTGGCCCCCACTTCATGAAGCTCATCCAGCTGTGACATCAGCTACGTGTG
 TCTACGAGAACCTCAAGATCACCTTGGGCGTGCAGTCCGGGTGACGCGGGGAGGGCCGCGC
 GCAGTGGACTCGCTGATCTCTGGGCCGCGAGCTTGGGGTGTGCAGCATCTCATCTGTGGAATG
 TGCCAACACTAAGCTGTCTCGAGCCAAGCTGTGAACACCTAGACGCAACCCAGCGAGGGGT
 GGGGAGAGCTGGCAGGCCCAGGGCTTGTCTGCTGACCCAGACACCTCTGTTGTTCC
 AGCGAAGGACCAAGGCAATTCCTTAGGCTTCAGGCTCAGCAGCTTCGGGGCTCACATGTGTAA
 GGACAGGACATTTTCTCAGTGCTTGCCTGCCAATAGTGAAGTGTGAGGCTTGGCCGGCTTAGT
 TCTTCCATTTACCTTTCGAGCCAGCTTGGCTGCTGTGCTGAGTAAAGTGGGAGGAGGCTACAG
 ATCTCCCTGTGCCCTTGTGCTGCTTCCATCCATAATCCATGATGAAGGTGAGTCAAGTGGCCT
 CCCACATCCCAACCCCTGTGCTCAATCCATAATCCATGATGAAGGTGAGTCAAGTGGCCT
 CCGAGGCTGACTTCCCAACTACAGCATTGACGCCAATTTGGCTGTGAAGGAAGAGAAAG
 GATCTGGCTTGTGCTCAGTGGCATCTGAGCCTCTGATGGCTGGGCTCTCGGGCAGTGT
 TGGAGTGCAGGGGCTCGGCTGCTGCTGCTGCTGCACAGAAGCGAAGTGTCTGGGCTCA
 TGGTCTCTGAGCTGGCTGGACCTGTCAAGATGGGCCACCTCAGAAGCAAACTCACTG
 TCCCACTGTGECATGAGGCAAGTGGAGCACCATGTTGAGGGCGAAGGGCAGAGCTTTGT
 GTGTTCTGGGAGCGGAAGGAAAGGTGTGAGGCGCTTAATTATGGACTGTTGGGAAAGGG
 TTTTGTCCAGAAGCAAGCCGGACAAATGAGCGACTTCTGTGCTCCAGAGGAAGACGAGG
 GAGCAGGAGCTTGGCTGACTCTCAGAGTCTGTTCTGACGCCCTGGGGGTTCTGTCCAAC
 CCAGCAGGGCCGACGCGGACAGCCACATTCACCTTGTGTAAGTGTGAAGTGTGAACCTATT
 ATTTTGTATTTATTTGAACAGAGTTATGTCTTAACATATTTTATAGATTTGTTTAAATATA
 GCTGTGATTTTCAAGTTCATTTTATTCATTTATGTTGTTGATGTGATCTGCCCTCCC
 AAGCCCGCCCAAGTGGGATGGGAGGAGGAGGAGAAGGGGGGCTTGGGCGCTGCACTACAT
 CTGTCCAGCAAAATTCCTTTTGGACTGGAGGCAGAAAGCGGCCAGGACAGACGCTG
 GCTCGTTTCTTGGCAGGTTTGGGGAAGGGCTTGGCCCGAGCTTAGGATTTACAGGTTTGA
 CTGGGGGCTGGAGAGAGAGGGAACCTCAATAACCTGAAGGTGGAATCCAGTATTATTC
 CTGCGCTGCGAGGTTTCTTTATTTTCACTCTTTTCTGAATGTCAAGGCAGTGAAGTGCCTCT
 CACTGTGAATTTGTGTGGCGGGGGCTGGAGGAGGGGTGGGGGGCTGGCTCCCTCC
 CAGCCTCTGTGCTGCCCTTGTCTTAACAATGCCGGCCAACTGGCGACCTACGGTTGCACCTCC
 ATTCACCAAGATGACCTGATGAGGAAATCTTCAATAGGATGCAAGATCAATGAAATTT
 GTTATATATGAACATAATACCTGGAGTCTGCAAAAAGCAATTAAGAAGAATTTGACGTTAG
 AAGTTGTCTATTTAAGGACCTCTTAATAAAGTTGTTTCAAAGCTGAAAAAATAAAAAA
 AA

FIGURE 206

MLCLCLYVPVIGEAEQTEFQYFESKGLPAELKSIFKLSVFIPSQEFSTYRQWKQKIVQAGDKD
 LDGQLDFEEFVHYLQDHEKKRLVFKILDKKNDGRIDAQEIMQSLRDLGVKISEQQAEEKILK
 SMDKNGTMTIDWNEWRDYHLLHPVENIPEIILYWKHSTIFDVGENLTVPDEFTVEERQTGMW
 WRHLVAGGGAGAVSRTCTAPLDRCLKVLMQVHASRSNNMGIVGGFTQMIREGGARSLWRGNGI
 NVLKIAPESAIFMAYEQIKRLVGSDQETLRIHERLVAGSLAGAIQSSIYPMEVLKTRMAL
 RKTGQYSGMLDCARRILAREGVAAFYKGYVPNMLGIIPYAGIDLAVYETLKNWLQHYAVNS
 ADPGVFVLLACGTMSSTCGQLASYPLALVRTRMQAQASIEGAPEVTMSSSLFKHILRTEGAFG
 LYRGLAPNFMKVIPAVSISYVVYENLKITLGVQSR

Important features:**Signal peptide:**

amino acids 1-16

Transmembrane domain:

amino acids 284-304, 339-360, 376-394

Mitochondrial energy transfer proteins signature.

amino acids 206-215, 300-309

N-glycosylation site.

amino acids 129-133, 169-173

Elongation Factor-hand calcium-binding protein.

amino acids 54-73, 85-104, 121-140

FIGURE 207

GGAAGGCAGCGGCAGCTCCACTCAGCCAGTACCCAGATACGCTGGGAACCTTCCCCAGCCAT
 GGCTTCCCTGGGGCAGATCCTCTTCTGGAGCATAATTAGCATCATATTATTCTGGCTGGAG
 CAATTGCACTCATCATTTGGCTTTGGTATTTTCAGGGAGACACTCCATCACAGTCACTACTGTC
 GCCTCAGCTGGGAACATTGGGGAGGATGGAATCCTGAGCTGCACTTTTGAACCTGACATCAA
 ACTTCTGATATCGTGATACAATGGCTGAAGGAAGGTGTTTTAGGCTTGGTCCATGAGTTCA
 AAGAAGGCCAAAGATGAGCTGTGCGAGCAGGATGAAATGTTTTCAGAGGCCGGACAGCAGTGTTT
 GCTGATCAAGTGATAGTTGGCAATGCCTCTTTGCGGCTGAAAAACGTGCAACTCACAGATGC
 TGGCACCTACAAATGTTATATCATCACTTCTAAAGGCAAGGGGAATGTAACCTTGAGTATA
 AAAGTGGAGCCTTCAGCATGCCGGAAGTGAATGTGGACTATAATGCCAGCTCAGAGACCTTG
 CGGTGTGAGGCTCCCCGATGGTCCCCCAGCCACAGTGGTCTGGGCATCCCAAGTTGACCA
 GGGAGCCAACTTCTCGGAAGTCTCCAATACCAGCTTTGAGCTGAACTCTGAGAATGTGACCA
 TGAAGGTTGTGTCTGTGCTCTACAATGTACGATCAACAACATACTCCTGTATGATTGAA
 AATGACATTGCCAAAGCAACAGGGGATATCAAAGTGACAGAATCGGAGATCAAAGGCCGGAG
 TCACCTACAGCTGCTAAACTCAAAGGCTTCTCTGTGTCTCTTCTTTCTTTGCCATCAGCT
 GGGCACTTCTGCCTCTCAGCCCTTACCTGATGCTAAAA**TAA**TGTGCGCTTGGCCACAAAAAAG
 CATGCAAAGTCATTGTTACAAACAGGGATCTACAGAATATTTCACCACCAGATATGACCTAG
 TTTTATATTTCTGGGAGGAAATGAATTCATATCTAGAAGTCTGGAGTGAGCAAACAAGAGCA
 AGAAACAAAAAGAAGCCAAAGCAGAAGGCTCCAATATGAACAAGATAAATCTATCTTCAA
 GACATATTAGAAGTTGGGAAAAATAATTCATGTGAAGTGAACAAGTGTGTTAAGAGTGATAAG
 TAAATGCACGTGGAGACAAGTGATCCCCAGATCTCAGGGACCTCCCCCTGCCTGTACCT
 GGGGAGTGAGAGGACAGGATAGTGCATGTTCTTTGTCTCTGAAATTTTATGTTATATGTGCTG
 TAATGTTGCTCTGAGGAAGCCCTGGAAAGTCTATCCCAACATATCCACATCTTATATCCA
 CAAATTAAGCTGTAGTATGTACCCTAAGACGCTGCTAATTGAGTGCCACTTCGCAACTCAGG
 GCGGCTGCATTTTAGTAATGGGTCAAATGATTCACTTTTTATGATGCTTCCAAGGTGCCT
 TGGCTTCTCTTCCAAGTACAAATGCCAAAGTTGAGAAAAATGATCATAATTTTAGCATAA
 ACAGAGCAGTCGGGGACACCGATTTTATAAATAAACTGAGCACCTTCTTTTAAACAAAAAA
 AA

[illegible]

210/330

FIGURE 210

MAASLGQVLALVLVAALWGGTQPLLKRASAGLQRVHEPTWAQQLQEMKTLFLNTEYLMPFLLNQCGLLYLTLASTDLTLAVPICNSLAIIFTLIVGKALGEDIGGKRKLDYCECGTQLCGSRHTCVSSFPEPISPEWVRTRFPFPLPFPLQLFCFLVAIRVFPFWTVWRKTEAGVWD

210/330

FIGURE 211

CTTCTGTAGGACAGTCACCAGGCCAGATCCAGAAGCCTCTCTAGGCTCCAGCTTTCTCTGTG
 GAAGATGACAGCAATTATAGCAGGACCTGCCAGGCTGTGAAAAAGATTCCGCAATAAACT
 TTGCCAGTGGGAAGTACCTTAGTGAACGCGCTAAGATGCCACTTCTTCTCATGTCCCAGGCT
 TGAGGCCCTGTGGTCCCCATCCTTGGGAGAAGTCAGCTCCAGCACCATGAAGGGGCATCCTCG
 TTGCTGGTATCACTGCAGTGCTTGTGTCAGCTGTAGAATCTCTGAGCTGCGTGCAGTGTAAT
 TCATGGGAAAAATCCTGTGTCAACAGCATTGCCTCTGAATGTCCCTCACATGCCAACACCAG
 CTGTATCAGCTCCTCAGCCAGCTCCTCTCTAGAGACACCAGTCAGATTATACCAGAATATGT
 TCTGCTCAGCGGAGAAGTGCAGTGAGGAGACACACATTACAGCCTTCACTGTCCACGTGTCT
 GCTGAAGAACACTTTTCATTTTGTAAAGCCAGTGCTGCCAAGGAAAGGAATGCAGCAACACCAG
 CGATGCCCTGGACCTCCCTGAAGAACGTGTCCAGCAACGCAGAGTGCCCTGCTTGTATTG
 AATCTAATGGAAGTTCCTGTGTCGTGGGAAGCCCTGGAAATGCTATGAAGAAGAAGTGTGTC
 TTTCTAGTTGCAGAACTTAAGAATGACATTGAGTCTAAGAGTCTCGTGCTGAAAGGCTGTTC
 CAACGTCACTAACGCCACCTGTCAAGTTCCTGTCTGGTGAAACAAAGACTCTTGGAGGAGTCA
 TCTTTTCGAAAGTTTGAGTGTGCAAATGTAAACAGCTTAACCCCCACGCTCTGCACCAACCACT
 TCCCAACAAGTGGGCTCCAAAGCTTCCCTCTACCTCTTGGCCCTTGCCAGCCTCCTTCTTCG
 GGGACTGCTGCCCTGAAGTCTGGGGCTGCACTTTGCCAGCACCCCATTTCTGCTTCTCTG
 AGGTCCAGAGCACCCCTGCGGTGCTGACACCCTCTTCCCTGCTCTGCCCCGTTTAACTGC
 CCAGTAAGTGGGAGTCACAGGTCTCCAGGCAATGCCGACAGCTGCCTTGTTCTTCATTATTA
 AAGCACTGGTTCATTCACTGCCAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 212

MKGILVAGITAVLVAAVESLSCVQCNSWEKSCVNSIASECPSHANTSCISSASSSSLET PVR
 LYQNMFCSAENCSEETHITAFTHVHVSAAEEHFHFVSQCCQGKECSNTSDALDPPLKNVSSNAE
 CPACYESNGTSCRGKPKWCYEEEQCVFLVAELKNDIESKSLVLKGCSNVSNATCQFLSGENK
 TLGGVIFRKFEKANVNSLTPTSAPTTSHNVGSKASLYLLALASLLLRGLLP

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FIGURE 213

GGCCTCGGTTCAAACGACCCGGTGGGTCTACAGCGGAAGGGAGGAGCGAAGGTAGGAGGCA
GGGCTTGCCCTCACTGGCCACCCTCCCAACCCCAAGAGCCAGCCCC**ATG**TGCCCGCCGCCG
GCGCGCTGCTGTGGGTCTGCTGCTGAATCTGGGTCCCCGGCGCGGGGGCCCAAGGCCTG
ACCCAGACTCCGACCAGAAATGCAGCGGGTCAGTTTACGCTTTGGGGGCCCATGACCCGCAG
CTACCGGAGCACCGCCGGACTGGTCTTCCCCGGAAGACAAGGATAATCCTAGAGGACGAGA
ATGATGCCATGGCCGACGCCGACCGCCTGGCTGGACCAGCGGCTGCCGAGCTCTTGGCCGCC
ACGGTGTCACCGGCTTTAGCCGGTCGTCCGCCATTAACGAGGAGGATGGGTCTTCAGAAGA
GGGGTTGTGATTAATGCCGGAAGGATAGCACCAGCAGAGAGCTTCCAGTGCGACTCCCA
ATACAGCGGGGAGTTCAGCACGAGGTTTATAGCCAATAGTCAGGAGCCTGAAATCAGGCTG
ACTTCAAGCCTGCCGCGCTCCCCGGGAGGTCTACTGAGGACCTGCCAGGCTCGCAGGCCAC
CCTGAGCCAGTGGTCCACACCTGGGTCTACCCGAGCCGGTGGCCGTCAACCTCACCCACAG
CCATGCCATCTCTGAGGATCTGCGGCTGGTGCTGATGCCCTGGGGCCCGTGGCACTGCCAC
TGCAAGTCGGGCACCATGAGCCGGAGCCGGTCTGGGAAGCTGCACGGCCTTTCCGGGCGCCT
TCGAGTTGGGGCGCTGAGCCAGCTCCGCACGAGACACAAGCCTTGACCTATCAACAATGTCT
CCTGCAACCGACTTCGGGAAGAGTGCCCCCTGGACACAAGTCTCTGTACTGACACCAACTGT
GCCTCTCAGAGCACCACCAGTACCAGGACCACCATAACCCCTTCCCCACCATCCACCTCAG
AAGCAGTCCCAGCCTGCCACCCGCCAGCCCTGCCAGCCCTGGCTTTTGGAAACGGGTCA
GGATTGGCCTGGAGGATATTGGAATAGCCTCTCTTCAGTGTTACAGAGATGCAACCAATA
GACAGAAACAGAGG**TAA**TGGCCACTTCATCCACATGAGGAGATGTCAATCTCAACCTCT
CTTGCCCTTTCAATCCTAGCACCCACTAGATATTTTGTAGTACAGAAAAACAAAACCTGAAAA
CACAA

FIGURE 214

MVPAAGALLWVLLLNIGPRAAGAQGLTQTPTMQRVSLRFGGPMTRSYRSTARTGLPRKTRI
ILEDENDAMADADRLAGPAAAEELLAATVSTGFSRSSAINEEDGSSEEGVVINAGKDSTSREL
PSATPNTAGSSSTRFIANSQEPEIRLTSSLPRSPGRSTEDLPGSQATLSQWSTPGSTPSRWP
SPSPTAMPSPEDLRLVLMWPWGPWHCHCKSGTMSRSRSGKLHGLSGRLRVGALSQLRTEHKPC
TYQQQPCNRLREECPLDTSLCDTNCASQSTTSTRTTTTPFPTIHLRSSPSLPPASPCPALA
FWKRVRIGLEDIWNSLSSVFTEMQPIDRNQR

FIGURE 215

CCCGGCTCGACCCACGCGTCCGGGGAGAAAGC**ATG**CCCGGCGCTGGCGGCGCGGTGGTCTGCTAGCTGGGGCA
 GCGGCGCTGGCGAGCGGCTCCAGGGCGACCGTGAAGCCGCTGTACCGCGACTGCGTACTGCAAGTGGCAAGAGCA
 GAACCTGCTCTGGGGGCGCTCTGAATCACTTCCGCTCCCGCCACCAATCTACATGAGTCTACAGCGGTGGACCT
 GTCGGGACGACTGAAGTATGAGTGATGTGGGTACCGCTTACCTCCAGAGGCTACCAAAAGTGCGCT
 CAGTTCATGGCAAGTGGCCCTTCTCCCGGTTCTGTTCTTTCAAGAGCCGGCATCGGCCGTGGCCTGTGTTCT
 CAATGGCCTGGCAGCGCTGGTAGTGCTCTGCGCGTACCGCACCTTCGTGCCAGCGCTCTCCGCCCATCTACCCACA
 CCTGTGTGGCCTTGCCTGGGTGTCCTCAATGCATGGTCTGTGTCACAGTCTTCCACACCCAGGGACACTGAC
 CTCACAGAGAAAATGGACTACTTCTGTGCCTCCACTGTATCCTACACTCAATCTACCTGTGCTGGGTGAGGAC
 CGTGGGGCTGCAGACCCAGCTGTGGTCAGTGCCCTCCGGGCTCTCCTGCTGCTCATGCTGACCGTGACAGCTCT
 CCTACCTGAGCCTCATCCGCTTCGACTATGGCTACAACCTGGTGGCCAACTGGCTATTGGCCTGGTCAACGTG
 GTGTGGTGGCTGGCCTGGTGCTGTGGAAACGAGCGCGGCTGCCTACAGTGCAGCAAGTGCCTGGTGGTGGTCTT
 GCTGCTGCAGGGGCTGTCCCTGCTCGAGCTGCTTGACTTCCACCGCTCTTCTGGGTCTGGATGCCCATGCCA
 TCTGGCAGCATAGCAACATCCCTGTCCACGCTCCTCTTTTTCAGCTTTCTGGAAGATGACAGCGCTGTACCTGCTG
 AAGGAATCAGAGGACAAGTTCAAGCTGGACT**GGA**AGACCTTGAGCGAGTCTGCCCCAGTGGGGATCCTGCCCCC
 GCCTGCTGGGCTCCCTTCTCCCTCAACCTTTGAGATGATTTTCTCTTTTCACTTCTTGAACCTGGACATGA
 AGGATGTGGGCCAGAAATCATGTGGCCAGCCACCCCTGTTGGCCCTCACCAGCGCTGGAGTCTGTTCTAGGG
 AAGGCTCCAGCATCTGGGACTCGAGAGTGGGACGCGCTCTACCTCCTGGAGCTGAACCTGGGGTGGAACTGA
 GTGTGTTCTTAGCTCTACCGGAGGACAGCTGCCGTTTCTCCTCCACACGCGCTCCTCCACATCCCAAGCTG
 CCTGGCTGGGTCTGAAGCCCTCTGTCTACCTGGGAGACAGGGACACAGCGCTTAGGATACAGGGGGTCCC
 CTTCTGTTACCAACCCCACTCCTCCAGGACACCACTAGGTGGTGGTGGATGCTGTTGTTCTTTGGCCAGCCAA
 GGTTCACCGCGATTCTCCCATGGGATCTTGAGGGACCAAGCTGCTGGGATTGGGAAGGAGTTTCAACCTGACC
 GTTGCCCTAGCCAGGTTCCAGGAGGCTCACCATACTCCCTTTAGGGCCAGGGCTCCAGCAAGCCCAAGGGCA
 AGATCCTGTCTGCTGTCTGGTTGAGAGCGCTGCCACCGTGTCTGGGAGTGTGGGCCAGGCTGAGTGCATAGG
 TGACAGGCGCTGAGCATGGCGTGGGTGTGTGTGAGCTCAGGCTAGGCTGCGAGTGTGGAGAGCGGTGTTGT
 CCGGGAAGAGTGTGGCTTCAAAGTGTGTGTGTGTCAGGGGTGGGTGTGTAGCGTGGGTAGGGGAACGTGTG
 TCGCGTCTGTGGTGGCATGTGAGATGAGTGACTGCCGCTGATGTGTCCACAGTTGAGAGGTTGGAGCAGGAT
 GAGGGAATCCTGTCAACATCAATATCACTTGTGGAGCGCCAGCTCTGCCCAAGACCCACCTGGGCGGACAGC
 CAGGAGCTCTCATGGCCAGGCTGCCCTGTGTGATCTTCCCTGTCTGGTGCCCTTTGCCGCGCTCCTGCAAC
 CTCAAGGTTCCCAACACACACAGCTGCTCCAGAGCAGCCCTCGGAGGCAAGAGGAGGAAATGGGATGGC
 TGGGGCTCTCTCCATCCTCCTTTCTCCTTGCCCTGCGATGGCTGGCCTTCCCTCTCAAACCTCCTATTCCCT
 GCTGCCAGCCCTTTGCCATAGCTGATTTTGGGGAGGAGGAAGGGGATTTGAGGAGAAAGGGAGAAAGCT
 TATGGCTGGGTCTGGTTTCTTCCCTTCCAGAGGCTTACTGTTCCAGGTTGGCCCCAGGGCAGCAGGGCC
 ACATATGCTGTGCCCTGGTAAAGTGACCCCTGCCATTACAGCAGCCCTGGCATTTCTCTGCCCAAGG
 AATAGAATGGAGGAGCTCCAGAACTTTCCATCCCAAGGCACTCTCCGTGGTGAAGCAGACTGGATTTTTC
 CTCGTGCCCTGACCCCTTGTCCCTTTGAGGGAGGGAGCTATGCTAGGACTCCAACCTCAGGACTCGGGTG
 GCTTGGCTAGCTTCTTTTGATAGTAAACCTTTTAAAGTGGGAGGGTGGCAGGGATGTGCTTAATAAATCAA
 TTCCAGCTCAAAAAAAAAAAAAAAAAA

FIGURE 216

MAGLAARLVLLAGAAALASGSQGDREPVYRDCVLQCEEQNCSGGALNHFRSRQPIYMSLAGW
TCRDDCKYECMWVTVGLYLQEGHKVPQFHGKWPFSRFLFFQEPASAVASFLNGLASLVMLCR
YRTFVPASSPMYHTCVAFAWVSLNAFWSTVFHTRDTDLTEKMDYFCASTVILHSIYLCCVR
TVGLQHPAVVSAFRALLLMLTVHVSYSLSLIRFDYGYNLVANVAIGLVNVVWWLAWCLWNQR
RLPHVRKCVVVVLLQGLSLELLDFPPLFWVLDAHAIWHISTIPVHVLFFSFLEDDSLYLL
KESEDKFKLD

Important features:**Signal peptide:**

amino acids 1-20

Transmembrane domains:

amino acids 105-123, 138-156, 169-185, 193-209, 221-240, 256-272

N-glycosylation site.

amino acids 40-44

N-myristoylation site.

amino acids 43-49

CUB domain proteins profile.

amino acids 285-302

Amiloride-sensitive sodium channels proteins.

amino acids 162-186

[illegible]

FIGURE 218

MAPQSLPSSRMAPLGMMLGLLMAACFTFCLSHQNLKEFALTNPEKSSSTKETKETERKAEDEL
 DAEVLEVFHPHTEWQALPGQAVPAGSHVRLNLQTGEREAKLQYEDKFRNNLKGKRLDINTN
 TYTSQDLKSALAKFKEGAEMESSKEDKARQAEVKRLFRPIEELKKDFDELNVVVIETDMQIMV
 RLINKFNSSSSSLEEKIAALFDLEYYVHQMDNAQDLLSFGGLQVVINGLNSTEPLVKEYAAF
 VLGAAFSSNPKVQVEAIEGGALQKLLVILATEQPPLTAKKKVLFALCSLLRHFPYAQRQFLKL
 GGLQVLRITLVQEKGTVEVLAVRVVTLTYDLVTEKMFEEEEAEELTQEMSPEKLQQYRQVHLLPG
 LWEQGWCEITAHLLALPEHDAREKVLQTLGVLLTTCRDYRQDPQLGRTLASLQAEYQVLAS
 LELQDGEDEGYFQELLGSVNSLLKELR

Important features:**Signal peptide:**

amino acids 1-29

Hypothetical YJL126w/YLR351c/yhcX family protein.

amino acids 364-373

N-glycosylation site.

amino acids 193-197, 236-240

N-myristoylation site.

amino acids 15-21, 19-25, 234-240, 251-257, 402-408, 451-457

Homologous region SLS1 protein.

amino acids 68-340

FIGURE 219

TTCGGCTTCCGTAGAGGAAGTGGCGCGGACCTTCATTGGGGTTTCGGTTCCCCCCTTCCC
 CTTCCCCGGGGTCTGGGGGTGACATTGCACCGCGCCCTCGTGGGGTGCCTTGCACCCCCA
 CGCGGACTCCCCAGCTGGCGCGCCCTCCCATTTGCCTGTCTGGTCAAGCCCCACCCCC
 TTCCCACTGACCAGCCATGGGGGGTGCCTGTTTTTCGGCTGCACTTTCGTCGCCTCGGC
 CCGGCTTTCGCGCTTTTCTTGATCACTGTGGCTGGGACCGCTTCGGCTTATCATCTCGGT
 CGCAGGGGCATTTTTCTGGCTGGTCTCCCTGCTCCTGGCCCTCTGTGGTCTGGTTTCATCTGG
 TCCATGTGACCGACCGGTGATGCCCCGGCTCCAGTACGGCCCTCTGATTTTTGGTGGTGTCT
 GTCTCTGTCTTCTACAGGAGGTGTTCCGCTTTGCTTACTACAAGCTGCTTAAGAAGGCAGA
 TGAAGGGTTAGCATCGCTGAGTGAGGACGGAAGATCACCATCTCCATCCGCGAGATGGCCT
 ATGTTTCTGGTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCT
 GATGCACTTGGGCCAGGTGTGGTTGGGATCCATGGAGACTCACCTATTACTTCTGCACTTC
 AGCCTTCTGACAGCAGCCATTATCCTGCTCCATACCTTTTGGGGAGTTGTGTTCTTTGATG
 CCTGTGAGAGGAGACGGTACTGGGCTTTGGGCTGTGGTGGGAGTCACTTACTGACATCG
 GGACTGACATTCTGAACCCCTGGTATGAGGCCAGCTGCTGCCCATCTATGCACTCACTGT
 TTCCATGGGGCTCTGGGCTTCATCACAGCTGGAGGGTCCCTCCGAAGTATTACAGCGCAGCC
 TCTTGTGTAAGGACTGACTACCTGGACTGATCGCCTGACAGATCCCACCTGCTTGCACCTG
 CCCATGACTGAGCCAGCCAGCCCGGGTCCATTGCCACATTTCTGCTCTCTCTCTGCTC
 GGTCTACCCCACTACCTCCAGGGTTTTGCTTTTGTCTTTTGTGACCGTTAGTCTCTAAGCTT
 TACCAGGAGCAGCTGGGTTTCAAGCAGTCACTGCTGGTGGGTTTGAATCTGCACTTATCCC
 CACCACCTGGGGACCCCTTGTGTGTGTCAGGACTCCCCCTGTGTGCTGCTGCTCTCAC
 CCTGCCAAGACTCACCTCCCTTCCCTCTGCAAGCCGACGGCAGGAGACAGTCCGGTGAT
 GGTGTATTCTGCCCTGCGCATCCACCCGAGGACTGAGGGAACTAGGGGGGACCCCTGGGC
 CTGGGGTGCCCTCCTGATGTCTCGCCCTGTATTTCTCCATCTCCAGTTCTGGACAGTGCAG
 GTTGCCAAGAAAAGGGACCTAGTTTAGCCATTGCCCTGGAGATGAAATTAATGGAGGCTCAA
 GGATAGATGAGCTCTGAGTTTCTCAGTACTCCCTCAAGACTGGACATCTTGGTCTTTTTTCTC
 AGGCCTGAGGGGGAAACCATTTTTGGTGTGATAAATACCTAACTGCCTTTTTTCTTTTTT
 GAGGTGGGGGGAGGGAGGAGGTATATGGAACCTTTCTAACCCTCCTGGGCTATATTTCTC
 TCCTCGAGTTGCTCCTCATGGCTGGGCTCATTTCGGTCCCTTTCTCCTTGGTCCAGACCTT
 GGGGGAAGGAAGGAAGTGATGTTTGGGAACCTGGCATTACTGGAACATATGGTTTTAACTC
 CCTTAACCACCAGCATCCCTCCTCTCCCCAAGGTGAAGTGAGGGTGTCTGTGGTGAAGTGC
 CACTCCAGAGCTGCAGTGCCTCAGTGGAGGAGTCACTACCATGACATCGTAGGGAAGGAGG
 GAGATTTTTTTGTAGTTTTTAATTTGGGGTGTGGGAGGGGCGGGGAGGTTTTCTATAAAGTGT
 ATCATTTTTCTGCTGAGGGTGGAGTGTCCATCCTTTTAATCAAGGTGATTGTGATTTTGACT
 AATAAAAAAGAATTTGTAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 220

MGAAVFFGCTFVAFGPAFALFLITVAGDPLRVIIILVAGAFFWLVSLLLASVVWFILVHVTDR
SDARLQYGLLIFGAAVSVLLQEVFRFAYYKLLKKADEGLASLEDGRSPISIRQMAYVSGLS
FGIISGVFSVINILADALGPGVVGIIHGDSPIYFLTSAFLTAAILLHTFWGVVFFDACERRR
YWALGLVVGSHLLTSGLTFLNPWYEASLLPIYAVTVSMGLWAFITAGGSLRSIQRSLCLKD



FIGURE 221

AAGCTGGTTTAAGGAAGCAGAGGAGGGTTAGATTGAGTGAGGACGGAAGATCAACCCA
 TTCCATTCCGCCAGATGGCCTATGTTTCTGGTCTCTCCCTTCGGNATCATCAGTGGTGTNT
 TNTCTGTTATCAATATTTTGGCTGATGCANTTGGGCCAGGTGTGGTTGGGATCCATGGAGAC
 TCACCCATTANTTCCTGANTTCAGCCTTTNTGACAGCAGCCATTATCCTGCTC

FIGURE 222

GACCGACCGTTCAGATGCCCGGTTCCAGTACGGCTTCCTGATTTTTGGTGCTGCTGTNCTG
TCCTTCTACAGGAGGTGTTCCGCTTTGCCTANTACAAGCTGCTTAAGAAGGCAGATGAGGGG
TTAGCATNGCTGAGTGAGGACGGAAGATCACCCATTTCCATCCGCCAGATGGCCTATGTTTN
TGGTNTTTCCTTCGGTATCATCAGTGGTGTNTTNTCTGTTATCAATATTTTGGNTGATGCAN
TTGGGCCAGGTGTGGTTGGGATCCATGGAGANTCACCCATTATAATTCCTGAATTCAGCCTTT
NTGACAGCAGCCATTATCCTGNTCCATACCTTTTGGGGAGTTGTGTTTTTTGATGCCTGTGA
GAGGAG

FIGURE 223

NGTTGGAGAAGTGGCGCGGACNTTCATTTGGGGTTTCGGTTTCCCCCCTTCCCTTTCCCCG
 GGGTCTGGGGTGACATTGCACGGGCCCCCTCGTGGGGTCGCGTTGCCACCCACGCGGACTCC
 CCAGNTGGNGCGCCCTTCCCATTGCTGTCTGGTCAGGCCCCACCCCCCTTCCACNTG
 ACCAGCCATGGGGGCTGCGGTGTTTTTCGGCTGCACCTTCGTGCGGTCGGCCCCGGCCTTCG
 CGCTTTTCTTGATCACTGTGGCTGGGGACCCGCTTCGCGTTATCATCCTGGTCGCAGGGGCA
 TTTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGAC
 CGACCGGTCAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTTGGTGCTGCTGTCTCTGTCC
 TTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTTA
 GCATCGCTGAGTGAGGACGGAAGATCACCCATCTCCATCCGCCAGATGGCCTATGTTTCTGG
 TCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTTGGCTGATGCACTTG
 GGCCAGGTGTGGTTGGGATCCATGGAGACTACCC



FIGURE 224

GTAAAAGAAAGTGGCCGGACCTTCATTGGGGTTTCGGTCCCCCTTTCCCNNTCCCCGGGG
TCTGGGGGTGACATTGCACCGCGCCCNTCGTGGGGTCGCGTTGCCACCCACGCGGACTCCC
CAGNTGGCGCGCCCCTCCCATTTGCCCTGTCTGGTCAGGCCCCACCCCCCTTCCACCTGA
CCAGCCATGGGGGCTGCGGTGTTTTTCGGGCTGCACCTTCGTGCGGTTGCGGCCCGGCCTTC
GCGCTTTTCTTGATCACTGTGGCTGGGGACCGCTTCGCGTTATCATCCTGGTCGAGGGGC
ATTTTCTGGCTGGTCTCCCTGCTCCTGGCCTCTGTGGTCTGGTTCATCTTGGTCCATGTGA
CCGACCGGTGAGATGCCCGGCTCCAGTACGGCCTCCTGATTTTGGTGCTGCTGTCTCTGTC
CTTCTACAGGAGGTGTTCCGCTTTGCCTACTACAAGCTGCTTAAGAAGGCAGATGAGGGGTT
AGCATCGCTGAGTGAGGACGGAAGATCACCATCTCCATCCGCCAGATGGCCTATGTTTCTG
GTCTCTCCTTCGGTATCATCAGTGGTGTCTTCTCTGTTATCAATATTTGGCTGATGCACTT
GGGCCAGGTGTGGTTGGGATCCATGGAGAC

FIGURE 225

GCCCCAGGGAGCAGTGGGTGGTTATAACTCAGGCCCGGTGCCAGAGCCCAGGAGGAGGCAG
 TGGCCAGGAAGGCACAGGCTGAGAAGTCTGCGGCTGAGCTGGGAGCAAAATCCCCACCCCC
 TACCTGGGGGACAGGGCAAGTGAACCTGGTGAGGGTGGCTCAGCAGGCAGGGAAGGAGAGG
 TGCTGTGCGTCTGCACCCACATCTTTCTCTGTCCCCTCCTTGCCCTGTCTGGAGGCTGCT
 AGACTCCTATCTTCTGAATCTATAGTGCCTGGGTCTCAGCGCAGTGCCGATGGTGGCCCGT
 CCTTGTGGTTCTCTCTACCTGGGGAATAAGGTGCAGCGGCC**ATG**GCTACAGCAAGACCCC
 CCTGGATGTGGGTGCTCTGTGCTCTGATCACAGCCTTGCTTCTGGGGGTACAGAGCATGTT
 CTCGCCAACAAATGATGTTTCTGTGACACCCCTCTAACACCGTGCCCTCTGGGAGCAACCA
 GGACCTGGGAGCTGGGGCCGGGAAGACGCCCGGTGCGATGACAGCAGCAGCCGCATCATCA
 ATGGATCCGACTGCGATATGCACCCAGCCGTGGCAGGCCGCGCTGTTGCTAAGGCCAAC
 CAGCTCTACTGCGGGGCGGTGTTGGTGCATCCACAGTGGCTGCTCAGGCCGCCCACTGCAG
 GAAGAAAGTTTTCAGAGTCCGTCTCGGCCACTACTCCCTGTCAACAGTTTATGAATCTGGGC
 AGCAGATGTTCCAGGGGTCAAATCCATCCCCACCCCTGGCTACTCCACCCCTGGCCACTCT
 AACGACCTCATGCTCATAAACTGAACAGAAGAATTGTCCTCCACTAAAGATGTGAGACCCAT
 CAACGTCTCCTCTCATTGTCCCTCTGTGCGGACAAAGTGCTTGGTGTCTGGCTGGGGGACAA
 CCAAGAGCCCCCAAGTGCACCTCCCTAAGGTCTCCAGTGCTTGAATATCAGCGTGCTAAGT
 CAGAAAAGGTGCGAGGATGCTTACCCGAGACAGATAGATGACACCATGTTCTGCGCCGGTGA
 CAAAGCAGGTAGAGACTCTGCCAGGGTGATTCTGGGGGGCCTGTGGTCTGCAATGGCTCCC
 TGCAGGGACTCGTGTCTGGGGGAGATTACCCTTGTGCCCGGCCCAACAGACCGGGTGTCTAC
 ACGAACCTCTGCAAGTTCACCAAGTGGATCCAGGAAACCATCCAGGCCAACTCT**GA**GTGTCAT
 CCCAGGACTCAGCACACCGGCATCCCCACCTGCTGCAGGGACAGCCCTGACACTCCTTTTCAG
 ACCCTCATTCTTCCAGAGATGTTGAGAATGTTTCATCTCTCCAGCCCTGACCCCATGTCT
 CCTGGACTCAGGGTCTGCTTCCCCACATTGGGCTGACCGTGTCTCTCTAGTTGAACCTTG
 GAACAATTTCAAAATGTCCAGGGCGGGGGTTCGCTCTCAATCTCCCTGGGGCACTTTTCAT
 CCTCAAGCTCAGGGCCCATCCCTTCTCTGCAGCTCTGACCCAAATTTAGTCCAGAAATAAA
 CTGAGAAGTGGAAAAAAA

FIGURE 226

MATARPPWMWVLCALITALLGVTEHVLANNVSCDHPSNTVPSSGNQDLGAGAGEDARSDD
SSSRIINGSDCDMHTQFWQAALLLRPNQLYCGAVLVHPQWLLTAAHCRKKVFRVRLGHYSLS
PVYESGQQMFQGVKSI PHPGYSHPGHSNDLMLIKLNRRI RPTKDVRPINVSSHCP SAGTKCL
VSGWGTTKSPQVHF PKVLQCLNISVLSQKRCE DAYPRQIDDTMFCAGDKAGRDSCQGD SGGP
VVCNGSLQGLVSWGDYPCAREPNRPGVYTNLCKFTKWIQETIQANS

FIGURE 227

ATGGTCAACGACCGGTGGAAGACCATGGCGGCGCTGCCAACTTGAGGACCGGCGCGCGA
 CAAGCCGCGAGGCGCGAGCTGGCGCTACGTGCTGTGCACCGTGTCTGTGGCCCTGGCTGTGC
 TGGTGGCTGTAGCTGTACCGGTGCGGTGCTCTTCTGAACCAAGCCGACGCGCGGCGCAGC
 GCGCCCGCACTGTGCTCAGCACTGGGGCTGCCAGCGCCAAACAGCGCCCTGGTCACTGTGGA
 AAGGGCGGACAGCTCGCACTCAGCATCCTATTGACCGGCTGCCCGACCTCACCGACA
 GCTTCGCACGCTGGAGAGCGCCAGGCCTCGGTGCTGCAGGCGCTCAGACAGCACAGCGGC
 CAGCCACGGCTGGTGGCGAACAGGAGCAGAGCTGCTGGACACGCTGGCGCAGCAGCTGCC
 CGGCTGTCTGGCGGAGCTCAGAGCTGCAGACGGAGTGCATGGGGCTGCGGAAGGGGCAATG
 GCACGCTGGGGCAGGGCCTCAGCGCCCTGCAGAGTGAGCAGGCGCGCTCATCCAGCTTCTC
 TCTCAGAGCCAGGGGGCTGGGCGGGCCCGGCAACAGGCGCAGCTTCAGAGAGCGCCCTGCC
 GCAGAGGACCGGGGGCTGGGCGGGCCCGGCAACAGGCGCAGCTTCAGAGAGCGCCCTGCC
 GGGGAACCGGGCCCGGGGCTGTGCCACTGCTCCGGCCCGGAGACTGTCTGGACGTCCTC
 CTAAGCGGACAGCAGGACGATGGCGCTACTGCTGTCTTTCCACCCACTACCGGGCGGCTT
 CCGGTGTACTGTGACATGGCGCAGGAGCGGGCGGCTGGAGGCTTTTCAGCGCGGGGAGG
 ACGGCTCGGTGAACCTTCTTCGGGGCTGGGACGCGTACCGAGACGGCTTTGGCAGGCTCAC
 GGGGAGCACTGGCTAGGGCTCAAGAGGATCCACGCCCTGACCACACAGGCTGCCACGAGCT
 GCACGTGGACCTGGAGGACTTTGAGAATGGCAGCGCTATGCCCGTACGGGAGCTTCGGCG
 TGGGCTTGTCTCCGTGGCCCTTGAGGAAGACGGTACCGGCTCACCGTGGCTGACTATTCC
 GGCACGTGAGGCGACTCCCTCTGAAGCACAGCGCATGAGGTTCAACACCAAGGACCGTGA
 CAGCGACATTAGAGAAACAACTGTGCCGCTTCTACCGCGGTGCCCTGGTGGTACCGCACT
 GCCACGCTCCAACCTCAATGGGCAGTACCTGCGGGGTGCACAGCCCTCCATGCGCAGCGG
 GTGGAGTGTCTCTTGGACCGGCTGGCAGTACTCACTCAAGTTCTCTGAGATGAAGATCCG
 CGCGGTCCGGGAGCGCC**TAG**ACTGGTGCACTTGTCTTTGGCCCTGTCTGGTCTCTGTGC
 CCCATCCCCGACCCCACTTCACTCTTTTCGTGAATGTTCTTCCACCCACTGTGCCCTGGCGGAC
 CCCTCTCCAGTAGGAGGGGGCGGGCCATCCCTGACACGAAGCTCCCTGGGCGGTTGAAGT
 CACACATCGCTTCTCGCGCTCCCCACCCCTCCATTTGGCAGCTCACTGATCTCTTGCCCT
 TGCTGATGGGGCTGGCAACTTGAGGACAGAGAGCAGGGGGCAGACACCCCTGGAGTCTCT
 TGCTGTTTGGCGCTCCCTGGCAGGATGGTGGAGTCTGCCCCAGGCACCCCTGTGCCCTGCC
 GGCACAAATACCGGCAATTATGGGACAGAGAGCAGGGGGCAGACACCCCTGGAGTCTCT
 CTAGCAGATCTGGGGAATGTCAAGTCTCTCTGAGGTCAAGTCTGAGGCCAGTATCCTCCAG
 CCCTCCCAATGCCAACCCCAACCCGTTTCCCTGGTGCCAGAGAACCCCTCTCCCCAA
 GGGCTCAGCCTGGCTGTGGGCTGGGTGGCCCCATCCTACCAGGCCCTGAGGTCAAGGATGGG
 GAGCTGCTGCCTTTGGGACCCACGCTCCAAGGTGAGACCAAGTTCCCTGGAGGCCACCCAC
 CCGTGCCCCGCGAGGCTGGGGTCTGCAGTCTCTTACCTGCTGTGCCACCTGCTCTCTG
 TCTCAAATGAGGCCCAACCCATCCCCACCCAGCTCCCGGCCCTCTCCTTACCTGGGGCAGC
 CGGGGCTGCCATCCATTTCTCTGCTCTGGAAGGTGGGTGGGGCCCTGCACGCTGGGGCT
 GGACTGCTGCTTATGGGAAGCTCTTGGTTTCTGGGCTGGGGCTAGGCAGGGCTGGGATGAG
 GCTTGTACAAACCCCAACCAATTTCCAGGGACTCCAGGGTCTGAGGCCCTCCACAGGAGG
 GCCTTGGGGGTGATGACCCCTTCCCTGAGGTGGCTGTCTCCATGAGGAGGCCAACCCCTTGGC
 ATTGACGCTGGCCACTTGACCCAGGCCAGGCCCGGGCCGGCGAGTGGTCAAGGGACAGGGA
 CCACCTCAGCGGCAATGGGTCGGGGGGACTGGGGCACCAGACAGGCACCACTGGACA
 CTTTCTTGTGAATCTCCCAACACCCAGCAGCTGTCTATCCCACTCTTGTGTGCACACA
 TGCAAGGTGAGACCCGCGAGGCTCCAGGACCCAGGCCAAGGCGAGGCTGGAGCGGG
 TCTCAGCTGTCTGTGACGACGCTGGACCGGCTGCGTACGTCAGGCCAGATGAGGAGG
 CGGCTTTTCCAAAGGCTCTGTATGGGGGCTCCGAAAGGGCTGGAGTCAGCCTTGGGAGCT
 GCCTAGACGCTCTCTCGGGCAGGAGGGAGGTGGCTTCTCCAAAGGACACCCGATGGCA
 GGTGCCCTAGGGGTGTGGGGTTCGGTTCTCCCTTCCCTCCCAAGATTGTGCTTAAAA
 AACAAATAATTTGACTTGGCACCCTGGGGGTGGTGGGAGAGGCGGTGTGACCTGGCTCTC
 TGTCCAGTGGCCACCGAGTGCATCCATGGCGCAG

FIGURE 228

MVNDRWKTMGGAQLEDRPRDKPQRPSGCVLCTVLLALAVLLAVAVTGAVLFLNHAHAPGT
 APPPVVSTGAASANSALVTVERADSSHLSILIDPRCPDLTDSFARLESAQASVLQALTEHQA
 QPRLVGDQEQLLDTLADQLPRLARASELQTECMGLRKHGTLGQGLSALQSEQGRLIQLL
 SESQGHMAHLVNSVSDILDALQRDRGLGRPRNKADLQAPARGTRPRGCATGSRPRDCLDVL
 LSGQQDDGVYSVFPHTYPAGFQVYCDMRTDGGGWTVFQRRREDGSVNFFRGWDAYRDGFGRLT
 GEHWLGLKRIHALTTQAAYELHVDLEDFENGTAAYARYGSFGVGLFSVDPEEDGYPLTVADYS
 GTAGDSLKXSGMRFTTKDRSDHSENNCAAFYRGAWWYRNCHTSNLNGQYLRGAHASADG
 VEWSSWTGWQYSLKFSEMIRPVREDR

FIGURE 229

GCAGTCAGAGACTTCCCTGCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCT
 TGCTTCTCTGAAGTAGCTCAGAGTAGCCCGCGGCCAGGGCAATCCGACCACATTTCACTCT
 CACCGCTGTAGGAATCCAG**ATG**AGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATG
 ATGGGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACTCGGGCATCCAGAGCCC
 CGGCGCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCTGTGAC
 TTTGTGCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTTCAGTACTACC
 AGCTCTCCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAGATTAGGAAATACGTCC
 CAAGAGTTGCAATCTCTTCAAGTCCAGAATATAAAGCTTGCAAGGAGTCTGCAGCATGTGGC
 TGA AAAAATCTGTCGTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAG
 AACAATGGAATGGCATGGAGACAATTGCTACCAAGTCTATAAAGACAGCAAAAGTTGGGAG
 GACTGTAAATATTTCTGCCTTAGTGAAAACCTACCATGCTGAAGATAAACAACAAGAAGA
 CCTGGAATTTGCGCGCTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTT
 TGGCGCCCTGACAGTGGCAAGGCCCTGGCTGTGGATGGATGGAACCCCTTCACTTCTGAACTG
 TTCCATATTATAATAGATGTCACCAGCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGG
 GATGATCTTCTCAAAGGACTGCAAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAA
 TGGTGAAGCCAGAGAGCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACT**TGA**TTTCGCC
 CTCGCAACTACAAATAGCAGAGTGAGCCAGGCGGTGCCAAGCAAGGGCTAGTTGAGACAT
 TGGGAAATGGAACATAATCAGGAAAGACTATCTCTCTGACTAGTACAAAATGGGTTCTCGTG
 TTTCTCTGTTGAGGATCACCAGCATTCTGAGCTTGGGTTTATGACGTATTTTAACAGTCA
 AGAAGTCTTATTATACATGCCACCAACCAACCTCAGAAACCCATAATGTCATCTGCGCTTGTG
 GCTTAGAGATAACTTTTAGCTCTCTTTCTTCTCAATGTCTAATATCACCTCCCTGTTTTCAT
 GTCTTCTTTACTACTTGGTGGAAATAAGAAACTTTTTGAAGTAGAGGAAATACATTGAGGTAAC
 ATCCTTTTCTCTGACAGTCAAGTAGTCCATCAGAAATTGGCAGTCACTTCCCAGATTGTACC
 AGCAAATACACAAGGAATCTTTTTGTTGTTTCAGTTCTACTAGTCCCTTCCAATCCAT
 CAGTAAAGACCCCATCTGCCTTGTCCATGCCGTTTCCCAACAGGGATGTCAGTTGATATGAG
 AATCTCAAATCTCAATGCCTTATAAGCATTCTTCTGTGTCCATTAAGACTCTGATAATTG
 TCTCCCTTCCATAGGAATTTCTCCAGGAAAGAAATATATCCCATCTCCGTTTCATATCAG
 AACTACCGTCCCCGATATTCCCTCAGAGAGATTAAAGACCAGAAAAAAGTGAGCCTCTTCA
 TCTGCACCTGTAATAGTTTCAGTTCTATTTTCTTCCATTGACCCATATTTATACCTTTTCAG
 GTACTGAAGATTTAATAATAATAAATGTAATACTGTGAAAAA

Figure 1 illustrates the experimental setup. A subject is seated at a table, looking at a video screen. A camera is positioned above the screen to record the subject's view. A light source is positioned to the left of the screen to illuminate the scene. A scale bar is shown below the screen to provide a reference for the size of the objects. The diagram is labeled with 'Subject', 'Video Screen', 'Camera', 'Light Source', and 'Scale Bar'.

Figure 1 illustrates the experimental setup. A subject is seated at a table, looking at a video screen. A camera is positioned above the screen to record the subject's view. A light source is positioned to the left of the screen to illuminate the scene. A scale bar is shown below the screen to provide a reference for the size of the objects. The diagram is labeled with 'Subject', 'Video Screen', 'Camera', 'Light Source', and 'Scale Bar'.

FIGURE 231

AATTTTCACCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGNTGG
ATGATGATGGGACACCACCATGAGCCTGCATTNTCAAGCTTTTGCCACAATTCGGCATCCAG
AGCCCCGGCGCACAGAGCACAGGGNTCCTTTTCAACGTGGCGACCAGTGGCCCTGACCCTG
CTGACTTTGTGCTTGGTGTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTCAGTA
CTACCAGCTCTCCAATACTGGTCAAGACACCATTCTCAAATGGAAGAAAGATTAGGAAATA
CGTCCCAAGAGTTGCAATTTNTTCAAGTCCAGAATATAAAGCTTGAGGAAGTNTGCAGCAT
GTGGCTGAAAAACTCTGTCGTGAGCTGTATAACAAAGCTGGAGGAAGTTTGAAGGAGGGCAA
AGTNTCCTCATNTACTATACACACCACTTCCC

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FIGURE 232

GCGGAGCGCAAGAACCTTGCAGCCAGAGCAGCTGCTGGAGGGGAATCGAGGCGCGGCTC
 CGGGGATTCGGCTCGGGCCGCTGGCTCTGCTCTGCGGGGAGGAGCGGGCCCGCCGCGGGG
 CCCGAGCCCTCCGGATCCGCCCCCTCCCGGTTCCCGCCCCCTCGGAGACTCCTCTGGCTGCT
 CTGGGGGTTTCGCGGGGCGGGGACCGCGGCTCGGGGCGCC**ATg**CGGGCATCGCTGCTGCTG
 TCGTGTCTGCGGGCCCGAGGGCCCGTGGCCGTGGGCATCTCCCTGGGCTTACCCGTAGCCGT
 GCTCAGCTCAGCTTGGTGGAGGAGCCGTGCGGCCAGGCCCGCCCCAACCTGGAGACTCTG
 AGCTGCCCGCGCGGCAACACCAGCGGCGCGCGGCCCAACTCGGTGCAGCCCGAGCG
 GAGCGCGAGAAGCCCGGGGCCGGAAGGCGCGGGGAGAATTGGAGCCGCGCTCTTGCC
 CTACCACCTGCACAGCCCGGCCAGGCCGCCAAAAAGGCCGTACGAGCCCGCTACATCAGCA
 CGGAGCTGGGCATCAGGCAGAGGCTGCTGGTGGCGGTGCTGACCTCTCAGACCACGCTGCC
 ACGCTGGGCGTGGCCGTGAACCGCAGCGTGGGGCACCGGCTGGAGCGTGTGGTGTTCCTGAC
 GGGCGCACGGGGCCCGCGGGCCCCACCTGGCATGGCAGTGGTGACGCTGGGCGAGGAGCGAC
 CCATTGGACACCTGCACCTGGCGCTGCGCCACCTGCTGGAGCAGCACGGCGACGACTTTGAC
 TGGTCTCTCTGGTGCCTGACACCACTACACCGAGGGCGACGGCCCTGGCACGCCCTAACTGG
 CCACCTCAGCCTGGCCCTCCGCGGCCACCTGTACTTGGGCCGGCCCCAGGACTTATCGGCG
 GAGAGCCCAACCCCGCCCGCTACTGCCACGGAGGCTTTGGGGTGTGCTGTGCGCGCATGCTG
 CTGCAAACTCGCGCCCCACTTGGAAAGGCTGCCCAACGACATCTGTCAGTGGCGGCCCTGA
 CGAGTGGCTGGTGTGCTGCATTCTCGATGCCACCGGGGTGGGCTGCACTGGTGACCACGAGG
 GGGTGCATATAGCCATCTGGAGCTGAGCCCTGGGGAGGCCAGTCAGGAGGGGGACCCTCAT
 TTTCCGAAGTGCCCTGACGCCCAACCCCTGTGCGTGCACCTGTGCACATGTACCAGTGCACAA
 AGCTTTCGCCCCAGGCTGAACCTGGAACGCACGTACCAGGAGATCAGGAGTTACAGTGGGAGA
 TCCAGAATACAGCCATCTGGCCGTTGATGGGGACCGGGCAGCTGCTGGCCCGCTGGGTATT
 CCAGCACCATCCCGCCCGGCTCCCGCTTTGAGGTGCTGCGCTGGGACTACTTCACGGAGCA
 GCACGCTTTCTCTGCGCCGATGGCTCACCCCGCTGCCACTGCGTGGGGCTGACCCGGGCTG
 ATGTGGCCGATGTTCTTGGGGACAGCTCTAGAGGAGCTGAACCGCGCTTACCACCCGGCCTTG
 CGGCTCCAGAAGCAGCAGCTGGTGAATGGCTACCGACGCTTTGATCCGGCCCGGGTATGGA
 ATACACGCTGGACTTGCAGCTGGAGGCACTGACCCCCAGGGAGGCCCGCGGCCCTCCTC
 GCGGAGTGCGAGCTGCTCCGGCCGCTGAGCCCGCTGGAGATCTTGCTGTGCCCTATGTCCT
 GAGGCGCTCAGCTCTCAGTGTGCTGCTGCCCTAGCTGCGGCTGAGCGTGACCTGGGCCCTTG
 CTTCTTGGAGGCTTTTGCCACTGCAGCCTGGAGCCTGGTGATGCTGCGGCAGCCCTGACCC
 TGCTGTACTGTATGAGCCCGGCCAGGCCAGCGCTGGCCATGCAGATGTCTTCGCACTT
 GTCAGGGCCACGTGGCAGAGCTGGAGCGGCGCTTTCCCGGTGCCCGGGTGCCATGGCTCAG
 TGTGCAGACAGCCGCAACCTCACCACTGCGCCTCATGGATCTACTCTCAAAGAAGCACCCGC
 TGGACACACTGTTCTCTGCTGGCCGGGCCAGACACGGTGCTCAGCGCTGACTTCTTGAACCCG
 TGCCGCACTGCATGCCATCTCCGGCTGGCAGGCTTCTTTCCATGCAATTTCCAAGCTTCCA
 CCCAGGTGTGGCCCCACCACAAGGGCTTGGGCCCCAGAGCTGGGCCGTGACACTGGCCGCT
 TTGATTCGCCAGGCAGCCAGGAGGCTGCTTCTACAACCTCCGACTACGTGGCAGCCCTGGG
 CGCTTCGGCGCAGCCTCAGAACAAGAAGAGGAGCTCTGGAGAGCCCTGGATGTGTACGAGCT
 GTTCTCCACTTCTCCAGTCTGCATGTGCTGCGGGCGGTGGAGCCGCGCTGCTGCGAGCGCT
 ACCGGGCCAGCAGCTGACAGCGCAGGCTCAGTGAGGACCTGTACCAACCGCTGCTCCAGAGC
 GTGCTTGAGGGCCCTCGGCTCCCGAACCCAGCTGGCCATGCTACTCTTTGAACAGGAGAGGG
 CAACAGCAGCT**Tg**ACCACCTGTCCCGTGGCCGTGGCATGGCCACACCCCAACCCCACTT
 CTCGCCAAAACAGAGCCACTGCCAGCCTCGCTGGGCAAGGCTGGCCGTAGCCAGAGCCCC
 AAGCTGGGCCACTTGGTCCCTCTCTGGCTCTGTGGTCCCTGGGCTCTGGACAAGCACTGGG
 GGAGCTGCCCCAGAGCCACCCACTTCTCATCCCAAAACCACTTCCCTGCCCCCTGACGCT
 GCTGATTCGGGCTGTGGCCCTCCACGTATTTATGCAGTACAGCTTGCCTGAGCCGACCCCTGC
 CTCCTGGGCCCTGGGGCTGGGCTGTAGAAGAGTTGTTGGGAAGGAGGAGCTGAGGAGGGG
 GCATCTCCAACCTTCTCCCTTTTGGACCTGCCGAAGCTCCCTGCCCTTAATAAACTGGCCA
 AGTGTGGAAAAA

FIGURE 233

MRASLLLSVLRPAGPVAVGISLGFTLSLLSVTWEEPCGPGPPQPGDSELPFRGNTNAARRP
NSVQPGAEREKPGAGEGAGENWEPRVLPYHPAQPGQAACKAVRTRYISTELGIRQLLVAVL
TSQTTLPTLGVAVNRTLGHRLERVVFLTGARGRRAPPGMAVVTLGEERPIGHLHLALRHLE
QHGDDEFWFFLVPDTTYTEAHGLARLTGHLSLASAAHLYLGRPQDFIGGEPTPGRYCHGGFG
VLLSRMLLQQLRPHLEGCRNDIVSARPDEWLGRCLDATGVGCTGDHEGVHYSHLELSPGEP
VQEGDPHFRSALTAPVRDPVHMYQLHKAFARAEELERTYQEIQELQWEIQNTSHLAVDGDRA
AAWPVGIPAPSRPASRFEVLRWDYFTEQHAFSCADGSPRCPLRGADRADVADVLGTALEELN
RRYHPALRLQKQQLVNGYRRFDPARGMEYTLDLQLEALTPOGGRPLTRRVQLLRPLSRVEI
LPVPYVTEASRLTVLLPLAAAERDLAPGFLEAFATAALEPGDAAAALTLLLLYEPRQAQRVA
HADVFAPVKAHVAELERRFPGARVPWLSVQTAAPSPRLMDLLSKKHPLDTLFLLAGPDTVL
TPDFLNRCRMHAISGWQAFPMHFQAFHPGVAPPQGPPELGRDTGRFDRQAASEACFYNS
DYVAARGRLAAASEQEEELLESLDVYELFLHFSSLVLRRAVEPALLQRYRAQTCSARLSEDL
YHRCLQSVLEGLGSRTOQLAMLLFEQEQGNST

FIGURE 234

GCTCTGGCCGGCCCCGGCGATTGGTCACCGCCCGCTAGGGGACAGCCCTGGCCTCCTCTGAT
 TGGCAAGCGCTGGCCACCTCCCCACACCCCTTGCGAACGCTCCCCTAGTGGAGAAAAGGAGT
 AGCTATTAGCCAATTCGGCAGGGCCCGCTTTTGAAGCTTGATTTCTCTTTGAAGATGAAAG
 ACTAGCGGAAGCTCTGCCTCTTTCCCCAGTGGGCGAGGGAACTCGGGGCGATTGGCTGGGAA
 CTGTATCCACCCAAATGTCACCGATTTCTTCTATGCAGGAAATGAGCAGACCCATCAATAA
 GAAATTTCTCAGCCTGGCCGAAAATGGTTGGCCCCACGAAGCCACGACAACCTGGAGGCAAAG
 AGGGTTGCTCAACGCCCCGCCTCATTGGAAAACCAAATCAGATCTGGGACCTATATAGCGTG
 GCGGAGGCGGGGCGATGATTGTCGCGCTCGCACCCACTGCAGCTGCGCACAGTCGCATTCTT
 TTCCCCGCCCCCTGAGACCCTGCAGACCATCTGTC**ATG**GCGGCTGGGCTGTTTGGTTTGAGC
 GCTCGCGTCTTTTGGCGGCAGCGGCGACGCGAGGGCTCCCGGCCGCCGCGTCCGCTGGGA
 ATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCTGTGGCGGGAAGCGGCCCCAGAAC
 CGACCACACCGTGGCAAGAGGACCCAGAACCCGAGGACGAAACTTGTATGAGAAGAACCCA
 GACTCCCATGTTATGACAAGGACCCCGTTTGGACGCTGGAACATGCGACTTGTCTTCTT
 CTTTGGCGTCTCCATCATCTTGGTCTTGGCAGCACCTTGTGGCCCTATCTGCCTGACTACA
 GGATGAAAGAGTGGTCCCGCCGGAAGCTGAGAGGCTTGTGAAATACCGAGAGGCCAATGGC
 CTTCCCATCATGGAATCCAACCTGCTTCGACCCAGCAAGATCCAGCTGCCAGAGGATGAG**TG**
ACCAGTTGCTAAGTGGGGCTCAAGAAGCACCGCCTTCCCCACCCCTGCCTGCCATTCTGAC
 CTCTTCTCAGAGCACCTAATTAAAGGGGCTGAAAGTCTGAA

GGCGGCTGGGCTGTTTGGTTTGAGCGCTCGCCGCTCTTTGGCGGCAGCGGCAGCGAGGGC
TCCGGCGCGCCCGCTCCGCTGGGAATCTAGCTTCTCCAGGACTGTGGTCGCCCCGTCCGCT
GTGCGGGGAAGCGGCCCCAGAACGCACACACGTTGCAAGAGGACCAGAACCCAGGA
CGAAAACTGTATGAGAAGAACCCAGACTCCCATGGTTATGACAAGACCCCGTTTTGGACG
TCTGGAACATGCGACTTGTCTTCTTCTTTGGCGTCTCCATCATCCTGGTCTTGGCAGCACC
TTTGTGGCCTATCTGCCTGACTACAGGATGAAAGAGTGGTCCCGCCGCGAAGCTGAGAGGCT
TGTGAAATCCAGAGAGCCCAATGGCCTTCCCATCATGGAATCCAAC TGCTTCGACCCAGCA
AGATCCAG

FIGURE 237

GCGGCGGCT**ATG**CCGCTTGCTCTGCTCGTCTGTTGCTCCTGGGGCCCGGCGGCTGGTGCCT
 TGCAGAACCCCCACGCGACAGCCTGCGGGAGGAACTTGTATACCCCCGTGCCTTCCGGGG
 ACGTAGCCGCCACATTCCAGTTCGCGCAGCGCTGGGATTCGGAGCTTCAGCGGGAGAGAGTG
 TCCCATTACAGGCTCTTTCCAAAGCCTGGGGCAGCTGATCTCCAAGTATTCTCTACGGGA
 GCTGCACCTGTCAATTCACACAAGGCTTTTGGAGGACCCGATACTGGGGCCACCCCTTCTGTC
 AGGCCCCATCAGGTGCAGAGCTGTGGTCTGGTTCGAAGACACTGTCACTGATGTGGATAAA
 TCTTGGAGGAGCTCAGTAATGTCCTCTCAGGATCTTCTGCGCCTCTCTCAACTTCATCGA
 CTCACCAACACAGTCACTCCCACTGCCTCCTTCAAACCCTGGGTCTGGCCAATGACACTG
 ACCACTACTTTCTGCGCTATGCTGTGCTGCCGCGGAGGTGGTCTGCACCGAAAACCTCACC
 CCCTGGAAGAAGCTCTTGCCCTGTAGTTCGAAGGCAGGCCCTCTCTGTGCTGCTGAAGGCAGA
 TCGCTTGTTCACACCAGTACCACTCCAGGCAGTGCATATCCGCCCTGTTTGAGAAATG
 CACGCTGTACTAGCATCTCCTGGGAGCTGAGGCAGACCCCTGTCACTTGATTTGATGCCTTC
 ATCACGGGGCAGGGAAGAAAGACTGGTCCCTCTTCCGGATGTTCTCCGAACCCCTCACGGA
 GCCCTGCCCCCTGGCTTCAGAGAGCCGAGTCTATGTGGACATCACACCTACAACCAGGACA
 ACGAGACATTAGAGGTGCACCCACCCCGACCACTACATATCAGGACGTATCCTAGGCACT
 CGGAAGACCTATGCCATCTATGACTTGCTTGACACCGCCATGATCAACAACCTCTCGAAACCT
 CAACATCCAGCTCAAGTGAAGAGACCCCGAGAGATGAGGCCCCCACTGCCCTTCTCTGC
 ATGCCAGCGGTACGTGAGTGGCTATGGGCTGCAGAAGGGGGAGCTGAGCACATCGCTGTAC
 AACACCCACCCATACCGGGCCTTCCCGGTGCTGCTGCTGGACACCGTACCCCTGGTATCTGCG
 GCTGTATGTGCACACCCTACCATCACCTCCAAGGGCAAGGAGAACAAACCAAGTTACATCC
 ACTACCAGCCTGCCAGGACCGGCTGCAACCCACCTCCTGGAGATGCTGATTACAGCTGCCG
 GCCAACTCAGTCACCAAGGTTTCCATCCAGTTTGAGCGGGCGCTGCTGAAGTGGACCGAGTA
 CACGCCAGATCCTAACCATGGCTTCTATGTACGCCCATCTGTCTCAGCGCCCTTGTGCCCA
 GCATGGTAGCAGCCAAAGCAGTGGACTGGGAAGAGAGTCCCCTCTTCAACAGCCTGTTCCCA
 GTCTCTGATGGCTCTAACTACTTTGTGCGGCTCTACACGGAGCCGCTGCTGGTGAACCTGCC
 GACACCGGACTTCAGCATGCCCTACAACGTGATCTGCCTCACGTGCACTGTGGTGGCCGTGT
 GCTACGGCTCCTTCTACAATCTCCTCACCCGAACCTTCCACATCGAGGAGCCCCGACAGGT
 GGCCTGGCCAAGCGGCTGGCCAACCTTATCCGGCGCGCCCGAGGTGTCCCCCACTCT**G**ATT
 CTTGCCCTTTCTCAGCAGCTGCAGCTGCCGTTTCTCTCTGGGAGGGGAGCCCAAGGGCTGTT
 TCTGCCACTTGCTCTCCTCAGAGTTGGCTTTTGAACCAAGTGCCCTGGACCAAGGTCAAGGC
 CTACAGCTGTGTTGTCCAGTACAGGAGCCACGAGCCAAATGTGGCATTTGAATTTGAATTA
 CTTAGAATTCATTTCTCACTGTAGTGGCCACCTCTATATTGAGGTGCTCAATAAGCAAA
 AGTGGTGGGTGGCTGCTGATTGGACAGCACAGAAAAAGATTTCATCACACAGAAAGGTC
 GGCTGGCAGCACTGGCCAAGGTGATGGGTGTGCTACACAGTGTATGTCACTGTGTAGTGA
 TGGAGTTTACTGTTTGTGGAAATAAAACGGCTGTTTCCGTGGAAAAA

FIGURE 238

MPLALLVLLLLGPGWCLAEPFPRDSLREELVITPLPSGDVAATFQFRTRWDSELQREGVSHY
RLFPKALGQLISKYSLRELHLSFTQGFWRTRYWGPPFLQAPSGAELWVWFQDVTVDVDSWK
ELSNVLSGIFCASLNFIDSTNTVPTASFVKPLGLANDTDHYFLRYAVLPREVVCENLTPWK
KLLPCSSKAGLSVLLKADRLFHTSYHSQAVHIRPVCRNARCTSI SWELRQTL SVVFDAFITG
QGKKDWSLFRMFRTLT EPCPLASESRVYVDITTYNQDNETLEVHPPPTTTYQDVILGRKT
YAIYDLLDTAMINNSRNLNIQLKWKRPPENEAPPVPFLHAQRYVSGYGLQKGELSTLLYNTH
PYRAFPVLLLDTPWPYLRLYVHTLTITSKGKENKPSYIHYQPAQDRLQPHLLEMLIQLPANS
VTKVSIQFERALLKWTEYTPDPNHGFYVSPSVLSALVPSMVAAPVDWEESPLFNSLFPVSD
GSNYFVRLYTEPLLVLNLTPTDFSPMPYNVICLTCTVVAVCYGSFYNNLTTRTFHIEEPRTGGLA
KRLANLIRRARGVPPL



FIGURE 239

CAACATGGGGTCCAGCAGCTTCTTGGTCCTCATGGTGTCTCTCGTTCTTGTGACCCTGGTGG
CTGTGGAAGGAGTTAAAGAGGGTATAGAGAAAGCAGGGGTTTGCCAGCTGACAACGTACGC
TGCTTCAAGTCCGATCCTCCCCAGTGTACACAGACCAGGACTGTCTGGGGAAAGGAAGTG
TTGTTACCTGCACGTGGCTTCAAGTGTGTGATTCTGTGAAGGAAGTGAAGAAGGAGGAA
ACAAGGATGAAGATGTGTCAAGGCCATACCCCTGAGCCAGGATGGGAGGCCAAGTGTCCAGGC
TCCTCCTCTACCAGGTGTCTCAGAAATTGATGCTGGGTCTTTTCTACCTCTGGGGTCACTC
TCACTTGGCACCTGCCCTGAGGGTCTTGAGACTTGGAATATGGAAGAAGCAATACCCAACC
CCACCAAAGAAAACCTGAGCTTGAAGTCTTTTCCCCAAAAGAGGAAGAGTCACAAAAG
TCCAGACCCAGGGACGGTACTTTCCCTCTCTACCTGGTGTCTCTCCTAATGCTCATGAAT
GGACCCCTCATGAATGAAACCAGTGCCCTTATAAGAGACCCCAAAGAGCTGCCTTGCCCTTC
TGCAATGTGTGATCACAGCTAGAAGGCACTGTGAGAGAAGAGAACTGGTCTCACCAGATG
CTGAATCTGCTGGTGCCTTGATCTTGACTTCCAGCCTCTAGAACTGTAAGAAATAAATAT
TTGCTGTTTATAATCCAA

FIGURE 240

MGSSSFVLVMSLVLVTLVAVEGVKEGIEKAGVCPADNVRCFKSDPPQCHTDQDCLGERKCC
YLHCGFKCVIPVKELEEGGNKDEDVSRPYPEPGWEAKCPGSSSTRCPQK

Signal sequence:

amino acids 1-19

N-myristoylation sites:

amino acids 23-29, 27-33, 32-38, 102-108

WAP-type 'four-disulfide core' domain signature:

amino acids 49-63



FIGURE 241

AAACCTCAGCACTTGCCGGAGTGGCTCATTTGTTAAGACAAAGGGTGTGCACTTCCTGGCCAGG
 AAACCTGAGCGGTGAGACTCCCAGCTGCCTACATCAAGGCCCCAGGACATGCGAACCCTTCC
 TCTAGAACCCGACCCACCACCA**ATG**AGGTCCTGCCTGTGGAGATGAGGCACCTGAGCCCAAGG
 CGTCCAGTGGTCTTGGCTTCTGGCTGTCTGGTCTTCTTTCTCTCGCTTGGCTTGCCTCTTTTA
 TTAAGGAGCCTCAAACAAAGCCTTCCAGGCATCAACGCACAGAGAACATTAAAGAAAGGTCT
 CTACAGTCCCTGGCAAAGCCTAAGTCCCAGGCACCCACAAAGGGCAGGAGGACAAACATCTTA
 TGCAGAGCCAGCGCCAGAGAACAATGCCCTCAACACACAAACCCAGCCCAAGGCCACACCA
 CCGGAGACAGAGGAAAGGAGGCCAACAGGCACCGCCGGAGGAGCAGGACAAAGGTGCCCCAC
 ACAGCACAGAGGGCAGCATGGAAGAGCCAGAAAAAGAGAAAAACATGGTGAACACACTGTCT
 ACCCAGAGGGCAAGATGCAGGGATGGCCTCTGGCAGGACAGAGGCACAATCATGGAAGAGCC
 AGGACACAAAGACGACCCAAAGGAATGGGGGCCAGACAGGAAGCTGACGGCCTCCAGGACG
 GTGTCAAGAGAAGCACCAGGGCAAAGCGGCAACCACAGCCAAAGACGCTCATTCCCAAAAGTCA
 GCACAGAATGCTGGCTCCACAGGAGCAGTGTCAACAAGGACGAGACAGAAAGGAGTGACCA
 CAGCAGTCATCCACACTAAGGAGAAGAAACCTCAGGCCACCCACCCCTGCCCTTTCCAG
 AGCCCCAGCAGCAGCAAGAACAAAGACTGAAGGCCGCCAACTTCAAATCTGAGCCTCGGTG
 GGATTTTGAAGAAAAATACAGCTTCGAAATAGGAGGCCCTCAGACGACTTGCCTGACTCTG
 TGAAGATCAAAGCCTCAAAGTCGCTGTGGCTCCAGAACTCTTTCTGCCAACCTCAGCTCT
 TTCCTGGACTCCAGACACTTCAACCAAGAGTGAGTGGGACCGCCTGGAACACTTTGCACACC
 CTTTGGCTTCTAGGAGCTCAACTACTCTTGGTGCAGAAGGTCGTGACACGCTTCCCTCCAG
 TGCCCCAGCAGCAGCTGCTCTTGGCCAGCCTCCCGCTGGGAGCCTCCGGTGACATCACTGT
 GCCGTGGTGGGCAACGGGGGCATCCTGAACAACTCCACATGGGCCAGGAGATAGACAGTCA
 CGACTACGTGTTCCGATTGAGCGGAGCTCTCATTAAAGGCTACGAACAGGATGTGGGGACTC
 GGACATCCTTCTACGGCTTTACCGCTTCTCCCTGACCCAGTCACTCCTTATATTGGGCAAT
 CGGGGTTTCAAGAAGCTGCCTCTTGGGAAGGACGTCCTGCTACTTGCCTTCCCTGGAAGGCAC
 CCGGACATATGAGTGGCTGGAAGCACTGCTTATGAATCAGACCGTGATGTCAAAGAACTTT
 TCTGGTTCAGGCACAGACCCAGGAAGCTTTTCCGGGAAGCCCTGCACATGGACAGGTACCTG
 TTGCTGCACCCAGACTTCTCCGATACATGAAGAACAGGTTTCTGAGGTCTAAGACCCCTGGA
 TGGTGCCCACTGGAGGATATACCGCCCACTGGGGCCCTCCTGCTGCTCACTGCCCCTTC
 AGCTCTGTGACCAGGTGAGTGTCTATGGCTTCATCACTGAGGGCCATGAGCGCTTTTCTGAT
 CACTACTATGATACATCATGGAAGCGGCTGATCTTTACATAAACCATGACTTCAAGCTGGA
 GAGAGAAGTCTGGAAGCGGCTACACGATGAAGGGATAATCCGGCTGTACCAAGCGTCCCTGGTC
 CCGGAACCTGCCAAAGCCAAAGAA**CTGA**CCGGGGCCAGGGCTGCCATGGTCTCCTTGGCTGCTC
 CAAGGCACAGGATACAGTGGGAATCTTGAGACTCTTTGGCCATTTCCATGGCTCAGACTAA
 GCTCCAAGCCCTTCAGGAGTTCCAAGGAACACTTGAACCATGGACAAGACTCTCTCAAGAT
 GGCAAATGGCTAATTGAGGTTCTGAAGTTCTTCAGTACATTGCTGTAGGTCTGAGGCCAGG
 GATTTTAAATTAATGGGGTGATGGGTGGCCAATACCACAATTCCTGCTGAAAAACACTCTT
 CCAGTCCAAAAGCTTCTTGATACAGAAAAAGAGCCTGGATTACAGAAACATATAGATCTG
 GTTTGAATCCAGATCGAGTTTACAGTTGTGAAATCTTGAAGGATTTACTTAACTTCACTAC
 AGATTGTCTAGAAGACTTTCTAGGAGTTATCTGATTCTAGAAGGCTATACCTTGTCTCTG
 TCTTTAAGCTATTTGACAACCTCTACGTGTTGTAGAAAACCTGATAATAATACAAATGATGTT
 GTCATGGAAAGGCAATAAATTTTCTACAGTGAAAAA

FIGURE 242

MRSLWRCRHLSQGVQWSLLAVLVFFLFALPSFIKEPQTKPSRHQRTENIKERSLQSLAKP
 KSQAPTRARRTTIYAEPAENNALNTQTQPKAHTTGDGRKEANQAPPEEQDKVPHTAQRAAW
 KSPEKEKTMVNTLSPRGQDAGMASGRTEAQSWKSQDTKTTOGNGGQTRKLTASRTVSEKHQ
 KAATTAKTLIPKSQHRMLAPTGAIVSTRTRQKGVTTAVIPPEKEKKQATPPAPFQSPTTQRN
 QRLKAANFKSEPRWDFEEKYSFEIGGLQTTCPDSVKIKASKSLWLQKLFPLNLTFLDSRHF
 NQSEWDRLEHFAPPFQGMELNYSLVQKVVTFRPPVQQQLLASLPAGSLRCITCAVVGNGG
 ILNNSHMQEIDSHDYVFRLSGALIKGYEQDVGTRTSFYGFATFSLTQSLILGNRGFKNVP
 LGKDVRYLHFLEGTRDYEWLEALLMNQTVMSKNLFWFRHRPQEAFFREALHMDRYLLHPDFL
 RYMKNRFLRSKTLDGAAHWRIYRPTTGALLLTALQLCDQVSAYGFITEGHERFSDHYDTSW
 KRLIFYINHDFKLEREVWKRHLHDEGIIRLYQRPGPGTAKAKN

Cytoplasmic Domain:

amino acids 1-10

Type II Transmembrane Domain:

amino acids 11-35

Lumenal catalytic Domain:

amino acids 36-600

Ribonucleotide Reductase small subunit Signature:

amino acids 481-496

N-glycosylation Sites:

amino acids 300-303, 311-314, 331-334, 375-378, 460-463

FIGURE 243

CGATGCGCGGACCCGGGCACCCCTCCTCCTGGGGCTGCTGCTGGTGGTGGGGCCTTCGCCG
GAGCAGCGAGTGGAATTTGTTCTCGAGATCTGAGGATGAAGGACAAGTTTCTAAAACACCT
TACAGGCCCTCTTTATTTTAGTCCAAAGTGCAGCAACACTTCCATAGACTTTATCACAACA
CCAGAGACTGCACCATTCCTGCATACTATAAAAGATGCGCCAGGCTTCTTACCCGGCTGGCT
GTCAGTCCAGTGTGCATGGAGGATAAGTGAGCAGACCGTACAGGAGCAGCACACCAGGAGCC
ATGAGAAGTGCCTTGGAAACCAACAGGGAAACAGAACTATCTTTATACACATCCCCTCATGG
ACAAGAGATTTATTTTGCAGACAGACTCTTCCATAAGTCCTTTGAGTTTTGTATGTTGTTG
ACAGTTTGCAATATATATTCGATAAATCAGTGTACTTGACAGTGTTATCTGTCACTTATTT

FIGURE 245

GGGCTGGGCCCCGCCGACGTCCAGCTGGCCGGCTTGGTCTGCGGTCCCTTCTCTGGGAGG
 CCCGACCCCGGCCGCGCCAGCCCCACCATGCCACCCGCGGGCTCCGCCGGGCCGCGCCG
 CTCACCGCAATCGCTCTGTTGGTGCTGGGGGCTCCCTGGTGCTGGCCGGCGAGGACTGCCT
 GTGGTACCTGGACCGGAATGGCTCCTGGCATCCGGGGTTTAACTGCGAGTTCTTCACCTTCT
 GCTGCGGGACCTGCTACCATCGGTACTGCTGCAGGGACCTGACCTTGCTTATCACCGAGAGG
 CAGCAGAAGCACTGCCTGGCCTTCAGCCCCAAGACCATAGCAGGCATCGCCTCAGCTGTGAT
 CCTCTTTGTGCTGTGGTTGCCACCACCATCTGCTGCTTCCTCTGTTCTGTTGCTACCTGT
 ACCGCCGGCGCCAGCAGCTCCAGAGCCCCATTTGAAGGCCAGGAGATTCCAATGACAGGCATC
 CCAGTGCAGCCAGTATACCCATACCCCCAGGACCCCAAAGCTGGCCCTGCACCCCCACAGCC
 TGGCTTCATGTACCCACCTAGTGGTCTGCTCCCCAATATCCACTCTACCCAGCTGGGCCCC
 CAGTCTACAACCCTGCAGCTCCTCCTCCCTATATGCCACCACAGCCCTCTTACCCGGGAGCC
TGAGGAACCAGCCATGTCTCTGCTGCCCTTTCAGTGATGCCAACCTTGGGAGATGCCCTCAT
 CCTGTACCTGCATCTGGTCTGGGGGTGGCAGGAGTCTCCAGCCACCAGGCCCCAGACCAA
 GCCAAGCCCTGGGCCCTACTGGGGACAGAGCCCCAGGGAAGTGAACAGGAGCTGAACTAGA
 ACTATGAGGGGTTGGGGGGAGGGCTTGGAATTATGGGCTATTTTTACTGGGGGCAAGGGAGG
 GAGATGACAGCCTGGGTACAGTGCCTGTTTTCAAATAGTCCCTCTGCTCCCAAGATCCCAG
 CCAGGAAGGCTGGGGCCCTACTGTTTGTCCTCTGGGCTGGGGTGGGGGGAGGGAGGAGGT
 TCCGTCAGCAGCTGGCAGTAGCCCTCCTCTCTGGCTGCCCCACTGGCCACATCTCTGGCCTG
 CTAGATTAAAGCTGTAAAGCAAAA

FIGURE 246

MPPAGLRRAAPLTAIALLVLGAPLVLAGEDCLWYLDNRNGSWHPGFNCEFFTFCGTCYHRYC
 CRDLTLLITERQQKHCLAFSPKTIAGIASAVILFVAVVATTICFLCSCCYLYRRRQQLQSP
 FEGQEIPMTGIPVQPVYPYQDPKAGPAPPQPGFMYPPSGPAPQYPLYPAGPPVYNPAAPP
 YMPQPSPSYFGA

Transmembrane Domains:

amino acids 10-28, 85-110

N-glycosylation Site:

amino acids 38-41

N-myristoylation Sites:

amino acids 5-10, 88-93



GGGGAGCTTAGGCCAGCGGCAGTGGTGGTGGGGCGGCGCAAGGGTGAGGGCGGGCCCGAGAA
CCCCAGGTAGGTAGAGCAAGAGAGATGCTGGTGTTCCTGCCCTCAAAATGGTCCCTTGCACCAACTG
TCATTTCCTACTTTCTCCTACCTGTGGGCTCTCTTAACCTGTGTCCACTCCTTCATGGTGTGCAGAG
CACTGAAGCACTCTCCAAATAGTAGTATGGGACACCAATTCCTTGGAAATAAAATACGACTTTC
CTGAGTACGTCTATCCAGGTCCTATGTATCTCTTGATCCATGCAAACTCTACCACGCTGACC
TTCTGGGAAACCCAGAAAGATAGAAATACAGCGCAGCTGACGCCACCACGACCATCATCTCCGA
TAGTCAACCACTGCGAGATATCTTAGGGCCACCTCGAGAAAGGGAGCTGGAGAGAGGCTATGCC
AAGAAACCCCTGCGAGGCTCTGGAAACACCCCTCTCAGGAGCAAAATGTGCATGCTGGCTCCCGAG
CGCTCTCTGTGGGGCTCCCGTACACAGTTGTCACTTCACTATGCTGGCAATCTTTCCGGAAG
TTTCTCGCGATTTTTACAAAGACCACTACAGAACCAAGGAAGGGGAACCTGAGGATATCATAGCAT
CAACCAATTTGAACCACTGCGAGCTAGAAATGGCTTTCCCTGGCTTTGATGAACCTGCTCTTC
TGACCAAGTCTCTCAATCAAAATAGAAAGAGCGCCAGGCACTAGGCATCTCCAAATATGCC
ATTGCTGAATCTGTGAGTCTGTGTGAGAGGACTCATGAAGAACCATTTTGATGTCACTGTGA
AGTGTAGCACTATCTGTGTGGCTCTCATATTTTCAGATTTTGAGTCTGTGACGACAGATAAAC
AGTGTGGTCTCAGGTTTGTGTATGCTGTGCCGAGACAAGGATAAATCAAGCAGGATATGCG
ACTCGAAGCTGTGGTGACTCTCTTATAGAAATTTATGAGATTTTGATGCAATACCGTATATCCCC
TGTGACCAATAGATATCTGTGCTATCTGCAATCTTCAGTCTGTGTGTGTGAAATACTGGGGA
TGACCAATATGACAGAAATCTGCTGTGTGTGTGATGCAAGAAAGCTCTCTGCATCAAGTAA
GCTTGGCTGTGAGTGTGCTGCTCCCATGAAGTGGCCCACTAGTGTTTGGGAAGCTGGTCA
CTATGAAATGGTGGCTATCTTGGTCAAAATGAGGATTTGCCAAATTTATGGAGTTTGTG
TCGTTGGTGGTGGTCTCTGAAATCAAAATGGAGATTTTCTTTGGCAAAGTTGTTTGA
CGGATGGAGGTAGATCTTTTGAATCTTCAACCTGTGTCTACACTGTGGAATACTCGT
CTCAGATCGGGAGTCTGTGATGATGTTTCTGATGAGGAGGCTTTATCTTGAATATG
CTAAGGGAGATCTTAGCGCTGACGCAATTTAAAGTGTATGTACAGTCTTTGATCAGAAGCA
TAGCTATAAAATACAAAAGAACGAGCACTGTGGGAGATGATGAGATTTTGGTACACCA
ATGTTGTAAGAGGGATGGATGGCTTTTGTCTAGAAGTCTTACCTCTACCTCCAT
TGGCATCAGGAAGGGGTGGATGTGAATCAATGATGAACACTTTGACCTGACAGGGGGT
TCCCTAATAACCATACAGTGAAGGGGAGGAATACACATGAACCAAGACCATCATGTA
AGGGCTCTGACGGCGCCCGGACACTTGGTACCTGTGGCATGTTCGATGACATCATCAC
AGCAATCAACATGTGCTCATGATTTTGTCAAAAACAAAACAGATGTGCTCATCTCC
AGAAGAGGTGGAATGGATCAAAATTAATGTGGGCATGAATGGCTATTACATGTGCATTACG
AGGATGATGGATGGGACTTTTGCATGGCTTTTAAAGGAACACACACGACGACTGACAGT
AATGATCGGGCAAGTCTATTAAACAATGCATTTCACTCTGACATTTGGGAAGCTGTCCAT
TGAAAGGGCTTGGATTTTATCCCTGTACTTTGAACATGAACGAAATATGCCGTGTCTT
AAGTTTGAATGAGCTGATTCCTATGTATAGTTTAAATGGAGAAAGAGATATGAATGAAGT
GAACTCAATTCAAGGCCCTCTCATGAGCTGTAAGGACCTCAATTGATGAAGCAGACTG
GACAGCAGAGGGCTCAGTCTCAGACCAATGCTGCGGAGTGAACTACTCTCCGCTGTG
TGACAACTCATACGCCGTGCGTACAGAGGCGAGAAGCTATTTCAGAAAGTGGAAAGGATCC
AATGGAAACTTGAGCTTGCCCTGTGACGCTGACCTTGGCAGTCTTTGCTGTGGGGCCCGAG
CAGAGAAGCTGGGATTTCTTTATAGTAATAATCAGTTTCTTTGTCAGTATGAGAAATC
GCAAAATGAAATTTGCCCTGTGCAAGAACCCAAATAAGGAAAGGCTTCAATGGCTACTAGAT
GAAAGCTTTAAGGAGATATAAATAAAACTCAGGAGTTTCCACAAATCTTCACTCAATGG
CAGAAACCCAGTAGGATACCCACTGGCCGTGCAATTTCTGAGGAAAACTGGAACAAACTTG
TACAAAAGTTTGAATCTTGGCTCATCTTCCATAGCCCAATGGTATGGGTACACAAATCAA
TTCTCCACAGCAACAGCGGTTGAAGAGGTTAAAGGATTTCTTGACGCTTTTGAAGAAATAG
TTCTCGAGCTCCGTTGTGTCCACAGACAAATGAAACCAATGAAGAAACATCGGTTGGATGG
ATAAGAAATTTGATAAAATCAGAGTGTGGCTGCAAGGTGAAAGGCTTGAAGCTATGTAA
TTCTCCCTTCCCGGTTCTCTTATCTTAATCAACCAACTTTGTTGAGTGTATTTTCA
CTAGAGATGGCTGTTTGGCTCCAATGAGATATGTTTCCCTTCAACTCATTTTGTGA
CATCTCCCTGTGAAAGAAATAGCTGTTAGTTTTCATGAATGGGCTTTTCATGAATGGCTA
TCCGTACCATGTGTTTGTTCATCAGAGTGTGCCCTGCAACTGAAACCAAGTGTGGGT
TCGCTGCCACAGAGAAATAAGTACCTTATTTCTTCAAAAATAAAATAAAATAAAATAA

FIGURE 248

MVFLPLKWSLATMSFLLSSLLALLTVSTPSWCQSTEASPKRSDGTPFPWNKIRLPEYVIPVH
 YDLLIHANLTTITFWGTTKVEITASQPTSTIILHSHHLQISRATLRKGAGERLSEEPLOVLE
 HPPQEIQIALLAPEPLLVGLPYTVVIHYAGNLSETFHGFYKSTYRTKEGELRILASTQFEPTA
 ARMAFPFCFDEPAFKASFISIKIRREPRHLAISNMPLVKSVTVAEGLIEDHFDVTVKMSTYLVA
 FIIISDFESVSKITKSGVKVSVYAVPDKINQADYALDAAVTLLEFYEDYFSIPYPLPKQDLAA
 IPDFQSGAMENWGLTTYRESALLFDAEKSSASSKLGITVTVAAHELAHQWFGNLVTMEWWNDL
 WLNEGFAKFMFVSVSVTHPELVGDYFFGKCFDAMEVDALNSSHPVSTPVENPAQIREMFD
 DVSYDKGACILNMLREYLSADAFKSGIVQYLQKHSYKNTKNEDLWDSMASICPTDGVKMGMDG
 FCSRSQHSSSSSHWHQEGVDVKTMMNTWTLQRGFPLITITVRGRNVHMKQEHYMKGSDGAPD
 TGYLWHVPLTFITSKSNMVHRFLKTKTDVLILPEEVEWIKFNVGMNGYYIVHYEDDGWDSL
 TGLLKGTHTAVSSNDRASLINNAFQLVLSIGKLSIEKALDLSLYLKHETEIMPFVQGLNELIP
 MYKLMEKRDMEVETQFKAFLIRLLRDLIDKQTTWDEGSVSEQMLRSELLLACVHNYQPCV
 QRAEGYFRKWKESNGNLSPVDVTLAVFAVGAQSTEGWDFLYSKYQFSLSSSTEKSQIEFALC
 RTQNKELQLWLLDESKFGDKIKTQEFQILTLIGRNPVGYPALWQFLRKNWNKLVQKFELGS
 SSIAHMVMGTTNQFSTRTRLEEVKGFFSSSLKENGSQLRCVQQTITETIENIGWMDKNFDKIR
 VWLQSEKLERM

Signal peptide:

amino acids 1-34

N-glycosylation sites:

amino acids 70-74, 154-158, 414-418, 760-764, 901-905

Neutral zinc metallopeptidases, zinc-binding region signature:

amino acids 350-360

FIGURE 249

CAGCCACAGACGGGTC**CATG**AGCGCGGTATTACTGCTGGCCCTCCTGGGGTTTCATCCTCCCAC
 TGCCAGGAGTGCAGGCGCTGCTCTGCCAGTTTGGGACAGTTACAGCATGTGTGGAAGGTGTCC
 GACCTACCCCGCAATGGACCCCTAAGAACACCAGCTGCGACAGCGGCTGGGGTGCCAGGA
 CACGTTGATGCTCATTGAGAGCGGACCCCAAGTGAGCCTGGTGCTCTCCAAGGGGTGCACGG
 AGGCCAAGGACCAGGAGCCCCGCGTCACTGAGCACCGGATGGGCCCCGGCCTCTCCCTGATC
 TCCTACACCTTCGTGTGCCGCCAGGAGGACTTCTGCAACAACCTCGTTAACTCCCTCCCGCT
 TTGGGCCCCACAGCCCCCAGCAGACCCAGGATCCTTGAGGTGCCAGTCTGCTTGTCTATGG
 AAGGCTGTCTGGAGGGGACAACAGAAGAGATCTGCCCCAAGGGGACCACACTGTTATGAT
 GGCCTCCTCAGGCTCAGGGGAGGAGGCATCTTCTCCAATCTGAGAGTCCAGGGATGCATGCC
 CCAGCCAGGTTGCAACCTGCTCAATGGGACACAGGAAATTGGGCCCGTGGGTATGACTGAGA
 ACTGCAATAGGAAAGATTTTCTGACCTGTCAATCGGGGACCACCATTTATGACACACGGAAC
 TTGGCTCAAGAACCCACTGATGGACCACATCGAATACCGAGATGTGCAGGTGGGGCAGGT
 GTGTCAGGAGACGCTGCTGCTCATAGATGTAGGACTCACATCAACCCCTGGTGGGGACAAAAG
 GCTGCAGCACTGTTGGGGCTCAAAATTCCCAGAAGACCACCATCCACTCAGCCCCCTCCTGGG
 GTGCTTGTGGCCTCCTATACCCACTTCTGCTCCTCGGACCTGTGCAATAGTGCCAGCAGCAG
 CAGCGTTCTGCTGAACTCCCTCCCTCCTCAAGCTGCCCTGTCCCAGGAGACCGGCAGTGTCT
 CTACCTGTGTGCAGCCCCCTTGGAACTGTTCAAGTGGCTCCCCCGAATGACCTGCCCCAGG
 GCGCCACTCATTTGTTATGATGGGTACATTCTCTCAGGAGGTGGGCTGTCCACCAAAAT
 GAGCATTAGGGCTGCGTGGCCCAACCTTCCAGCTTCTTGTGTTGAACCACACAGACAAATCG
 GGATCTTCTCTGCGCGTGAGAAGCGTGATGTGCAGCCTCCTGCCTCTCAGCATGAGGGAGGT
 GGGGCTGAGGGCCTGGAGTCTCTCACTTGGGGGGTGGGCTGGCACTGGCCCCAGCGCTGTG
 GTGGGGAGTGGTTTGGCCCTCCTGCT**TAA**CTCTATTACCCACAGATTCTTACCCTGCTGA
 CCACCCACACTCAACCTCCCTCTGACCTCATAACCTAATGGCCTTGGACACCAGATTCTTTC
 CCATTCTGTCCATGAATCATCTTCCCCACACACAATATTATATCTACTACCTAACAGCA
 AACTGGGGAGAGCCTGGAGCATCCGGACTTGCCTTATGGGAGAGGGGACGCTGGAGGAGTG
 GCTGCATGTATCTGATAATACAGACCTGTCTTTCA

FIGURE 250

MSAVLLLLALLGFIPLPLPGVQALLCQFGTVQHVKVSDLPQWTPKNTSCDSGLGCQDTLMLI
 ESGPQVSLVLSKGCTEAKDQEPRVTEHRMGPGLSLISYTFVCRQEDFCNNLVNSLPLWAPQP
 PADPGSLRCPVCLSMEGCLEGTTEEICPKGTTTHCYDGLLRRLGGGIFSNLRVQGCMPPQPGCN
 LLNGTQEIGPVGMTENCNRKDFLTCHRGTTIMTHGNLAQEPTDWTTSNTEMCEVGQVCQETL
 LLIDVGLTSTLVGTKGCSTVGAQNSQKTTIHSAPPGVLVASYTHFCSSDL CNSASSSSVLLN
 SLPPQAAAPVPGDRQCPTCVQPLGTCSSGSPRMTCPRGATHCYDGYIHLGGGLSTKMSIQGC
 VAQPSSFLNHNTRQIGIFSAREKRDVQPPASQHEGGGAEGLESITWGVGLALAPALWWGVVC
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FIGURE 251

GCGACGGGCAGGACGCCCCGTTTCGCCTAGCGCGTGCTCAGGAGTTGGTGTCTCGCTGCGCT
 CAGC**ATG**AGGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCCTGTCACTGCTG
 CCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTCGTCCCTGG
 CCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCGGACGGCCTGGAAGAGTCG
 GCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGGGTCTGTCAT
 GGAAAAATTGGTCCCATTTGGCTCTAAAGGTGAGAAAGGAGATTCCGGTGACATAGGACCCCC
 TGGTCCTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTGCGCAAGGCCATCGGGG
 AGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTCATCAAGAATGCTGTCGCC
 GGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAGGAGGAGAAGCGCTACGCGGA
 CGCCAGCTGTCTGCCAGGGCCGCGGGGCACGCTGAGCATGCCAAGGACGAGGCTGCCA
 ATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTGGCCCCTGTCTTCATCGGCATCAAC
 GACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGACCACTCCCCCATGCGGACCTTCAACAA
 GTGGCGCAGCGGTGAGCCCCAACATGCCTACGACGAGGAGGACTGCGTGGAGATGGTGGCCT
 CGGGCGGTGGAACGACGTGGCCTGCCACACCACCATGTACTTTCATGTGTGAGTTTGACAA
 GAGAACATCT**GCA**GCCTCAGGCTGGGGCTGCCATTGGGGGCCCCACATGTCCCTGCAGGGTT
 GGCAGGGACAGAGCCCAGACCATGGTGCCAGCCAGGGAGCTGTCCCTCTGTGAAGGGTGGAG
 GCTCACTGAGTAGAGGGCTGTTGTCTAAACTGAGAAAATGGCCTATGCTTAAGAGGAAAATG
 AAAGTGTTCCCTGGGGTGCTGTCTCTGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCA
 ATGTCAATTATGTAATTATTACCCAGAATTGCTCTTCCATAAAGCTTGTGCCTTTGTCCAAGC
 TATACAATAAAATCTTTAAGTAGTGCAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAAA

FIGURE 252

MRGNLALVGVLISLAFLSLLPSGHPQFAGDDACSVQILVPGLKGDAGEKGDKGAPGRPGRVG
PTGEKGMGDKGQKGSVGRHGKIGPIGSKGEKGDSDIGFPPGPNGEPGLPCECSQLRKAIGE
MDNQVSQLTSELKFIKNAVAGVRETESKIYLLVKEEKRYADAQLSCQGRGGTLSMPKDEAAN
GLMAAYLAQAGLARVFIGINDLEKEGAFVYSDHSPMRTFNKWRSGEPNNAYDEEDCVEMVAS
GGWNDVACHTTMYFMCEFDKENM

FIGURE 253

AGTGACTGCAGCCTTCCTAGATCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAG
 CACCAGTGTGTGAGGGGAGCAGGCAGCGGTCTAGCCAGTTCCCTTGATCCTGCCAGACCACC
 CAGCCCCCGGCACAGAGCTGCTCCACAGGCACCATGAGGATCATGCTGCTATTTCACAGCCAT
 CCTGGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGTGG
 TTCCCTGGCGGGGGCCGAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTC
 AAAAGCCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAA
 GGAATCAACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGA
 GGAGCGTCCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCTCGGCCC
 CTTTATCCCAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACC
 TTTATAAGACTCTCCTACGGATGTGAATCAAGAGAACGTCCCCAGCTTTGGCATCCTCAAGT
 ATCCCCCGAGAGCAGAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTC
 TTTCCCTGTCCAATCCCCAGGTGCGCAGCTCCTGTTACCTTTCTCTTCCCTGTTCTTGT
 AACATTCTTGTGCTTTGACTCCTTCTCCATCTTTTCTACCTGACCCTGGTGGAACATGCA
 TAGTGAATATCCCCAACCCCAATGGGCATTGACTGTAGAATACCTTAGAGTTCCCTGTAGTGT
 CCTACATTAAAAATATAATGTCTCTCTATTCCTCAACAATAAAGGATTTTTGCATATGAA
 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 254

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDL YQLLQRLFKSHSSLEGLLK
ALSQASTDPKESTSPKSRDMHDFVGLMGKRSVQPEGKTGFPLPSVRVPRPLHPNQLGSTGK
SSLGTEEQRPL

Important features:**Signal peptide:**

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

FIGURE 255

GGCGCTCTCCGGCTGCTCCTATTGAGCTGTCTGCTCGCTGTGCCCGCTGTGCCTGCTGTGCC
 CGCGCTGTGCGCGCTGCTACCGCTCTGCTGGACGCGGAGAGCCAGCGAGCTGGTGATTG
 GAGCCCTGCGGAGAGCTCAAGCGCCAGCTCTGCCCGCAGGAGCCAGGCTGCCCGGTGAGTC
 CCATAGTTGCTGCAGGAGTGGAGCCATGAGCTGCGTCCTGGGTGGTGCATCCCCCTTGGGGC
 TGCTGTTCTCTGGTCTGCGGATCCCAAGGCTACCTCCTGCCAACGCTCACTCTCTTAGAGGAG
 CTGCTCAGCAAATACCAGCACAACGAGTCTCACTCCCGGTCGCGAGAGCCATCCCCAGGGA
 GGACAAGGAGGAGATCCTCATGCTGCACAACAAGCTTCGGGGCCAGGTGCAGCCTCAGGCCT
 CCAACATGGAGTACATGGTGAGCGCCGGCTCCGGCCGAGAGGCTGGCACCCGGGGTGGGGC
 CTGGGCCACCGCCTGCTCTGTTCCCCAGCCAGCTCTGTTCCCCAGCCAGTGCGTGTGATGG
 CTGGCTCAGGGTCTCCTCTGGCAGGGGAGGATCCCGGCTCTGTTCTGTTTTGTTTGTGTT
 TTGAGACAGGGTCTCACTCTGCCACTGACGCTGGAGTGCAATGGCACAAATCGTCATGCCCTG
 AAACCTTAGACTCCCGGGTTAAGCGATCCTGCTTCAGCCTCCCAAGTAGCTGGAACACAG
 GCATGCACCATGGTGCCAGCTAGATTTTAAATATTTTGGGAGATGGGGGTCTTGCTACGT
 TGCCAGGCTGGTCTTGAACCTCCTAGGCTCAAGCAATCCTCCTGCCTCAGCCTCTCAAAGTG
 CTAGGATTATAGGCATGAGTCACCTGTCTGGCTCTGGCTCTGTTCTTAACATTCTGCCAAA
 ACAACACACGTGGGTTCCTGTGCAGAGCCTGCCTCGTTGCCTCATGTCACTCTTGGTAGC
 TCCACTGGGAACACAGCTCTCAGCCTTCCACCTGGAGGCAGAGTGGGGAGGGGCCAGGG
 CTGGGCTTTGCTGATGCTGATCTCAGCTGTGCCACACGCTAGCTGCACCACCTGACTTCTC
 CTTAGCCCGTGTGAGCCTCACTTTCCACTTGGAGAGTCCTTCCTCGCGTGGTTGCCATGACT
 GTGAGATAAGTCGAGGCTGTGAAGGGCCCGGCACAGACTGACCTGCCTCCCAACCCCTAGG
 CTTTGCTAACCGGAAAGGAGCTAACGGTGACAGAAGACAGCCAAGGTCAACCCCTCCCGGGT
 GATTGTGATGGGTGTTCCAGGTGTGGTTGGGCGATGCTGCTACTTGACCCCAAGCTCCAGTG
 TGGAACTTCCTTCTGGCTGGTTTTCCAGAACTACAGAGGAATGGACCACAGTCTTCAGG
 GTCCCTCCTCGTCCCAACCGGAGCCTCCACCTTGCCATCCGTGACGTATGAATGGCTT
 TTTAAACAAACCCAGTCCCAGCCTGGGTAACATGTTAAAGCCCGCTCTCTACAAAAAATC
 CAAGTTAGCCGGGCATGGTGTGCGCACCTGTAGTCCAGCTGCAAGTGGGACTGAGGTGGAG
 GTGGAGGTGGGGGGTGGGAGCTGAGGAAGGAGGATCGCTTGAGCCTGGGAAGTCGAGGCTGC
 AGTGAGCTGAGATTGCACCACTGCACTCCAGCCTGGGTGACAGAGCAAGACCCCTGTCTCAAAA

FIGURE 256

MSCVLGGV IPLGLLFLVCGSQGYLLPNVTLLLELLSKYQHNEHSRVRRAIPREDKEEILML
HNKLRGQVQPQASNMEYMVSA SGRRGWHRGWGLGHQPALFPSQLCSPASACDGWLRVSSGR
GGSRLCSVLFVCFETGSHSATDAGVQWHNRHALKP

Important features:

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 27-31, 41-45

N-myristoylation site.

amino acids 126-132, 140-146

Amidation site.

amino acids 85-89

FIGURE 257

AAGGAGAGGCCACCGGGACTTCAGTGTCTCCTCCATCCCAGGAGCGCAGTGGCCACT**ATG**GGG
GTCTGGGCTGCCCCCTTGTCCTCCTCTTGACCCCTCCTTGCGAGCTCACATGGAACAGGGCCGG
GTATGACTTTGCAACTGAAGCTGAAGGAGTCTTTTCTGACAAATTCCCTCCTATGAGTCCAGC
TTCCTGGAATTGCTTGAAAAGCTCTGCCTCCTCCATCTCCCTTCAGGGACCAGCGTCAC
CCTCCACCATGCAAGATCTCAACACCATGTTGTCTGCAACACA**TGA**CAGCCATTGAAGCCTG
TGTCTTCTTGCCCCGGGCTTTTGGGCCGGGGATGCAGGAGGCAGGCCCCGACCCCTGTCTTT
CAGCAGGCCCCACCCCTCCTGAGTGGCAATAAATAAAATTGCGGTATGCTG

FIGURE 258

MGSGLPVLLLTLLGSSSHGTGPGMTLQLKLKESFLTNSSYESSFLELLEKLCLLLHLPSTGTS
VTLHHARSQHHVVCNT

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FIGURE 259

AATTGTATCTGTGTAATGTTAAACAAACGAAATAAAATAGAAGGAAAACTTTCTGAGTTT
CAAAAACAACAGACTAGTACTCTAAAGAACTCTTTAAACAATTAAGTGTAGGATTGCAGT
TATGATTGGATATTATTTAATTCTGTTTCTGATGTGGGGTTCCTCCACTGTGTTCTGTGTGC
TATTAATATTTACCATTGCAGAAGCTTCATTCAGTGTGAAAATGAATGCTTAGTGGATCTG
TGCCTCTTACGCATATGTTACAAATTATCTGGAGTTCCTAATCAATGCAGAGTCCCCCTCC
CTCCGATTGTTCTAAAT**TAA**TTGAAAGATGTCTGCTGTGGAAAAAGGCATGTATTTAAATCTG
TATGATTCTCAACCATCTTTAGTTGGGAAAGTCCTTGAAAGCCAATGAAATACTTTTTTT
TTTTCTTGGCACTAATCAAGTGAGTGTACCTTTTCACTTAGTAGGATGTGTTGTTACGCTA
GTAAATAGAAACCTGTGTTTATTCTCAGGTATTTAGAAACAACAGCCATCATTTTATTTT
ATGTGTGTGTTCTTGGCTGTATTCATAAATTATATATTTTGGGCTATCAAATATTACTTCAT
TCAATATAAATAACAATAGTAGAAGTTGTTTACTTAGATATGCTTTCTAGTTGCATTTTCTC
AGCCTATGTAAGACTACTTTGTTGTAATAGCCTTTGAAATTTACAGTACTGTCTCTCTACTA
TCTTCAGATTACTTGATTCAAATAAACCAATTATGTTTGAATTGATATTAATAAAACCAGA
ATAAAAGTTCATATCTACCC

260/330

FIGURE 260

MIGYYLILFLMWGSSTVFCVLLIFTIAEASFVSENECLVDLCLLRICYKLSGVPNQCRVPLP
SDCSK

Important features:

Signal peptide:

amino acids 1-29

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FIGURE 261

GAGGATTTGCCACAGCAGCGGATAGAGCAGGAGAGCACCACGGAGCCCTTGAGACATCCTT
 GAGAAGAGCCACAGCATAAGAGACTGCCCTGCTTGGTGTTTTGCAGGATGATGGTGGCCCTT
 CGAGGAGCTTCTGCATTGCTGGTTCGTGCTTCCAGCTTTTCTGCCCCCGCCGAGGTGAC
 CCAGGACCCAGCCATGGTGCTTACATCTACCAGCGCTTTCGAGTCTTGGAGCAAGGGCTGG
 AAAAATGTACCAAGCAACGAGGGCATACATTCAAGAATTCGAAGAGTCTCAAAAATATATA
 TCTGTCTATGCTGGGAAGATGTCAGACCTACACAAGTGAGTACAAGAGTGCAGTGGGTAACTT
 GGCCTGAGAGTTGAACGTGCCCAACGGGAGATTGACTACATACAATACCTTCGAGAGGGCTG
 ACGAGTGCATCGTATCAGAGGACAAGACACTGGCAGAAATGTTGCTCCAAGAAGCTGAAGAA
 GAGAAAAAGATCCGGACTCTGCTGAATGCAAGCTGTGACAACTGCTGATGGGCATAAAGTC
 TTTGAAAATAGTGAAGAAGATGATGGACACACATGGCTCTTGGATGAAGAATGCTGTCTATA
 ACTCTCCAAGGTGTACTTATTAATTGGATCCAGAAACAACACTGTTTGGGAATTTGCAAAAC
 ATACGGGCACTTATGAGGATTAACACCAAGCCAGCTCCCCGGAAGCAAATCCTAACACTTTC
 CTGGCAGGGAACAGGCCAAGTGATCTACAAAGGTTTTCTATTTTTTCATAACCAAGCAACTT
 CTAATGAGATAATCAAAATATAACCTGCAGAAGAGGACTGTGGAAGATCGAATGCTGCTCCCA
 GGAGGGGTAGGCCGAGCATTGGTTTACCAGCACTCCCCCTCAACTTACATTGACCTGGCTGT
 GGATGAGCATGGGCTCTGGGCCATCCACTCTGGGCCAGGCACCCATAGCCATTGGTCTCTCA
 CAAAGATTGAGCCGGCCAGCTGGGAGTGGAGCACTTCACTGGGATACCCCATGCAGAAGCCAG
 GATGCTGAAGCCTCATTCCTCTTGTGTGGGTTCTCTATGTGGTCTACAGTACTGGGGCCCA
 GGGCCCTCATCGCATCACCTGCATCTATGATCCACTGGGCACTATCAGTGAGGAGGACTTGC
 CCAACTTGTCTTCCCCAAGAGACCAAGAAGTCACTCCATGATCCATTACAACCCAGAGAT
 AAGCAGCTCTATGCCTGGAATGAAGGAACACAGATCATTTACAAACTCCAGACAAGAGAAAA
 GCTGCCCTCTGAAGTAAATGCACTTACAGCTGTGAGAAGAGCACTGTGGCTTTGGCAGCTGTTT
 TACAGGACAGTGAGGCTATAGCCCTTCAACAATATAGTATCCCTCTAATCACACACAGGAAG
 AGTGTGTAGAAGTGGAATACGTATGCCTCCTTTCCCAAATGTCACTGCCTTAGGTATCTTC
 CAAGAGCTTAGATGAGAGCATATCATCAGGAAGTTTCAACAATGTCCATTACTCCCCAAA
 CCTCCTGGCTCTCAAGATGACCACATTCTGATACGCCCTACTTCAAGCCTTTTGTTTTACT
 GCTCCCCAGCACTTACTGTAACTCTGCCATCTTCCCTCCCACAATTAGAGTTGTATGCCAGC
 CCCTAATATTACCACCTGGCTTTTCTCTCCCCCTGGCCTTGTCTGAAGCTCTTCCCTCTTTTT
 CAAATGTCTATTGATATCTCCCATTTTCACTGCCCAACTAAAAATACTATTAAATATTCTTT
 CTTTTCTTTCTTTTTTTTGGAGCAAGGTCTCACTATGTTGCCAGGCTGGTCTCAAACTCC
 AGAGCTCAAGAGATCCTCCTGCCCTCAGCCTCCTAAGTACCTGGGATTACAGGCATGTGCCAC
 CACACCTGGCTTAAAACTACTATTTCTTATTGAGGTTTAACTCTATTTCCCCTAGCCCTGTC
 CTTCCACTAAGCTTGGTAGATGTAATAATAAAGTGAAAAATATTAACTATTGAATATCGCTTT
 CCAGGTGTGGAGTGTTTGCACATCATGAATTCCTGTTTCACTTTTGTGAAACATGCACAAG
 TCTTTACAGCTGCATTCTACAGTTTGTAGTGAGTAACACAATTTCAAAGTGAAAGATACAGC
 TAGAAAAATACTACAATCCCATAGTTTTTCCATTGCCCAAGGAAGCATCAATACGSTATGTT
 TGTTCACTACTCTTATAGTCAATGCGTTTCATGTTTCAAGCCTAAAAATATAGTCTGTCCC
 TTTAGCCAGTTTTTCATGTCTGCACAAGACCTTTCAATAGGCCTTTCAAATGATAATTCTCC
 AGAAAACAGTCTAAGGGTAGGACCCCAACTTAGCCTCCTCTTGTCTGTCTGTCTGTCTGT
 TTCTCTCTTTCTGCTTTAAATTCATAAAAGTGACACTGAGCAAAAAAAAAAAAAA

FIGURE 262

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FSKNISVMLGRCQTYTSEYKSAVGNLALRVERA~~Q~~REIDYIQYLREADECIVSEDKTLAEMLL
QEAE~~EE~~EKKIR~~T~~LLNASCDNMLGKSLKIVKKMMDTHGSWMKDAVYN~~S~~PKVYLLIGSRNNTV
WEFANIRAFMEDNTK~~P~~APRKQIL~~T~~LSWQGTGQVIYK~~G~~FLFFHNQATSNEIIKYNLQKRTVED
RMLLPGGVGRALVYQHSPSTYIDLAVDEHGLWAIHSGPGTHSHLVLT~~K~~IEPGTLGVEHSDWT
PCRSQDAEASFLCGVLYVVYSTGGQGPHRITCIYDPLGTISEEDLPNLFFPKRPRSHSMIH
YNPRDKQLYAWNEGNQIIYKLQTKRKLPLK

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FIGURE 263

GGGCGCCCGCTACTCACTAGCTGAGGTGGCAGTGGTTCCACCAAC**ATG**GAGCTCTCGCAGA
 TGTCGGAGCTCATGGGGCTGTCGGTGTGCTTGGGCTGCTGGCCCTGATGGCGACGGCGGGCG
 GTAGCGCGGGGGTGGCTGCGCGCGGGGGAGGAGAGGAGCGGCCGCGCCCTGCCAAAAAGC
 AAATGGATTTCACCTGACAAATCTTCGGGATCCAAGAAGCAGAAACAATATCAGCGGATTTC
 GGAAGGAGAAGCCTCAACAACACAACCTTCAACCACCGCCTCCTGGCTGCAGCTCTGAAGAGC
 CACAGCGGGAACATATCTTGCATGGACTTTAGCAGCAATGGCAAAATACCTGGCTACCTGTGC
 AGATGATCGCACCATCCGCATCTGGAGCACCACCAAGGACTTCTCGCAGCGAGAGCACCAGCA
 TGAGAGCCAACGTGGAGCTGGACCACGCCACCTGGTGCCTTCAGCCCTGACTGCAGAGCC
 TTCATCGTCTGGCTGGCCAACGGGGACACCCCTCCGTGTCTTCAAGATGACCAAGCGGGAGGA
 TGGGGGCTACACCTTCACAGCCACCCAGAGGACTTCCCTAAAAAGCACAAAGCGCCTGTCA
 TCGACATTGGCATTGTCTAACACAGGGAAGTTTATCATGACTGCCTCCAGTGACACCACTGTCT
 CTCATCTGGAGCTGAAGGGTCAAGTGTCTTACCATCAACACCAACCATGAACAACAC
 ACACGCTGCTGTATCTCCCTGTGGCAGATTGTAGCCTCGTGTGGCTTACCCACAGATGTGA
 AGGTTTGGGAAGTCTGCTTTGGAAAGAAGGGGAGTTCCAGGAGGTGGTGCAGCCTTCGAA
 CTAAAGGGCCACTCCGCGGCTGTGCACCTCGTTTGTCTTCCAACGACTCACGGAGGATGGC
 TTCTGTCTCCAAGGATGGTACATGAAACTGTGGGACACAGATGTGGAATACAAGAAGAAGC
 AGGACCCCTACTTGTCTGAAGACAGGCCCGCTTTGAAGAGCGCGCGGTGCCGCGCTGCCG
 CTGGCCCTCTCCGCCAACCGCCAGGTCTTGGCCTTGGCCAGTGGCAGTAGTATTCTCTCTA
 CAATACCCGCGCGGGCGAGAAAGGAGGAGTGTCTTGAAGCGGTCCATGGCAGTGTATCGCCA
 ACTTGTCTTTGACATCACTGGCCGCTTTCTGGCCTCCTGTGGGACCGGGCGGTGCGCGCTG
 TTTCAACAACACTCCTGGCCACCGAGCCATGGTGGAGGAGATGCAGGGCCACCTGAAGCGGGC
 CTCCAACGAGAGCACCCCGCAGAGGCTGCAGCAGCAGCTGACCCAGGCCCAAGAGACCCCTGA
 AGAGCCTGGGTGCCCTGAAGAAG**TGA**CTCTGGGAGGGCCCGGCGCAGAGGATTGAGGAGGAG
 GGATCTGGCCTCCTCATGGCAGCTGTGCCATCTTTCCTCCAGGTGGAAGCCTTTTCAGAAGG
 AGTCTCTGGTTTTCTTACTTGGTGGCCCTGCTTCTCCATTGAAACTACTCTTGTCTACTT
 AGGTCTCTCTCTTCTTGTGGCTGTGACTCCTCCCTGACTAGTGGCCAAGGTGCTTTTCTCTC
 CTCCAGGCCAGTGGGTGGAATCTGTCCCACTGGCACTGAGGAGAATGGTAGAGAGGAG
 AGGAGAGAGAGAGAGAATGTGATTTTGGCCTTGTGGCAGCACATCCTCACACCCAAAAGAG
 TTTGTAAATGTTCCAGAACACCTAGAGAACACCTGAGTACTAAGCAGCAGTTTTCAGGA
 TGGGAGACTGGGATAGCTTCCCATCACAGAAGTGTGTTCCATCAAAAAGACACTAAGGGATT
 TCCTTCTGGGCCCTCAGTTCCTATTGTGAAGATGGAGAATAATCCTCTCTGTGAACCTCTTGCA
 AAGATGATATGAGGCTAAGAGAATATCAAGTCCCAGGTCTGGAAGAAAAGTAGAAAAAGAT
 AGTACTATTGTCCAATGTCTATGAAAGTGGTAAAAGTGGGAACCAAGTGTGCTTTGAAACCAAA
 TTAGAAACACATTCTTGGGAAGGCAAGTTTCTGGGACTTGATCATACATTTTATATGGT
 TGGGACTTCTCTCTTGGGAGATGATATCTTGTTTAAGGAGACCTCTTTTCAGTTCATCAAG
 TTCATCAGATATTGAGTGCCCACTCTGTGCCAAATAATGAGCTGGGGATTAAAAAAA
 AA

FIGURE 264

MELSQMSELMGLSVLLGLLALMATAAVARGWLRAGEERSGRPACQKANGFPDPKSSGSKKQK
QYQRIRKEKPQQHNFTHRLAAALKSHSGNISCMDFSSNGKYLATCADDRTIRIWSTKDFLQ
REHRSMRANVELDHATLVRFSPDCRAFIVWLANGDTLRVFKMTKREDGGYTFTATPEDFPKK
HKAPVIDIGIANTGKFIMTASSDTTVLIWSLKGQVLSTINTNQMNNTAAVSPCGRFVASCG
FTPDVKVWEVCFGKKGEFQEVVRAFELKGHSAAVHSFAFSNDSRRMASVSKDGTWKLWDTDV
EYKKKQDPYLLKTGRFEEAAGAAPCRLALSPNAQVLALASGSSIHLYNTRRGEKEECFERVH
GECIANLSFDITGRFLASCGDRAVRLFHNTPGHRAMVEEMQGHLKRASNESTRQRLQQQLTQ
AQETLKSLGALKK

Important features:**Signal peptide:**

amino acids 1-25

N-glycosylation site.

amino acids 76-80, 92-96, 231-235, 289-293, 378-382, 421-425

Beta-transducin family Trp-Asp repeat protein.

amino acids 30-47, 105-118, 107-119, 203-216, 205-217, 296-308

FIGURE 265

TGGCCTCCCCAGCTTGCCAGGCACAAGGCTGAGCGGGAGGAAGCGAGAGGCATCTAAGCAGG
 CAGTGTTTTGCCCTTACCCCCAAGTGACCATGAGAGGTGCCACGCGAGTCTCAATCATGCTCC
 TCCTAGTAACTGTGTCTGACTGTGCTGTGATCACAGGGGCCTGTGAGCGGGATGTCCAGTGT
 GGGGCAGGCACCTGCTGTGCCATCAGCCTGTGGCTTCGAGGGGTGCGGATGTGCACCCCGCT
 GGGGCGGGAAGCGGAGGAGTGCCACCCCGGCAGCCACAAGGTCCCCTTCTTCAGGAAACGCA
 AGCACCCACACCTGTCTTGCTTGCCCAACCTGCTGTGCTCCAGGTTCCCGGACGCGAGGTAC
 CGCTGCTCCATGGACTTGAAGAACATCAATTTTTAGGCGCTTGCCCTGGTCTCAGGATACCCA
 CCATCCTTTTCTGAGCACAGCCTGGATTTTTATTCTGCCATGAAACCCAGCTCCCATGAC
 TCTCCAGTCCCTACACTGACTACCCTGATCTCTTGTCTAGTACGCACATATGCACACAG
 GCAGACATACCTCCCATCATGACATGGTCCCAGGCTGGCCTGAGGATGTCACAGCTTGAGG
 CTGTGGTGTGAAAGGTGGCCAGCCTGGTTCTCTTCCCTGCTCAGGCTGCCAGAGAGGTGGTA
 AATGGCAGAAAGGACATTTCCCTTCCCTCCCCAGGTGACCTGCTCTCTTTCTGGGCCCTG
 CCCCTCTCCCCACATGTATCCCTCGGTCTGAATTAGACATTCTTGGGCACAGGCTCTTGGGT
 GCATTGCTCAGAGTCCCAGGTCCTGGCCTGACCCTCAGGCCCTTCACGTGAGGTCTGTGAGG
 ACCAATTTGTGGGTAGTTTCATCTTCCCTCGATTGGTTAACTCCTTAGTTTCAGACCACAGAC
 TCAAGATTGGCTCTTCCCAGAGGGCAGCAGACAGTCACCCCAAGGCAGGTGTAGGGAGCCCA
 GGGAGGCCAATCAGCCCCCTGAAGACTCTGGTCCCAGTCAGCCTGTGGCTTGTGGCCTGTGA
 CCTGTGACCTTCTGCCAGAATTGTCATGCCTCTGAGGCCCCCTCTTACCACACTTTACCAGT
 TAACCCTGAAGCCCCCAATTCCACAGCTTTTCCATTAAATGCAAATGGTGGTGGTTCAA
 TCTAATCTGATATTGACATATTAGAAGGCAATTAGGGTGTTCCTTAAACAACCTCTTTCCA
 AGGATCAGCCCTGAGAGCAGGTGGTGACTTTGAGGAGGGCAGTCCTCTGTCCAGATTGGGG
 TGGGAGCAAGGGACAGGGAGCAGGGCAGGGCTGAAAGGGGCACTGATTAGACCAGGGAGG
 CAACTACACCAACATGCTGGCTTTAGAATAAAAGCACCAACTGAAAAA

266/330

FIGURE 266

MRGATRVSIMLLLVTVSDCAVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGECHP
GSHKVPFFRKRKHHTCPCLPNLLCSRFPDGRYRCSMDLKNINF

Signal peptide:

amino acids 1-19

Tyrosine kinase phosphorylation site:

amino acids 88-95

N-myristoylation sites:

amino acids 33-39, 35-41, 46-52

266/330

FIGURE 267

AGCGCCCGGGCGTCGGGGCGGTAAAAGCCGGCAGAGGGAGGCACTTGAGAA**ATG**TCTTTC
 CTCACGAGCCCAAGTTTCTTCACCATGGGGATGTGGTCCATTGGTGCAGGAGCCCTGGGGGC
 TGCTGCCCTTGGCATTGCTGCTTGCCAACACAGACGTGTTTCTGTCCAGCCCCAGAAAGCGG
 CCCTGGAGTACCTGGAGGATATAGACCTGAAAACACTGGAGAAGGAACCAAGGACTTTCAA
 GCAAAGGAGCTATGGGAAAAAAATGGAGCTGTGATTATGGCCGTGCGGAGGCCAGGCTGTTT
 CCTCTGTCGAGAGGAAGCTGCGGATCTGTCTCCCTGAAAAGCATGTTGGACCAGCTGGGCG
 TCCCCCTCTATGCAGTGGTAAAGGAGCACATCAGGACTGAAGTGAAGGATTTCCAGCCTTAT
 TTCAAAGGAGAAATCTTCTGGATGAAAAGAAAAAGTTCTATGGTCCACAAAGCGGAAGAT
 GATGTTTATGGGATTTATCCGCTCTGGGAGTGTGGTACAACCTTCTTCCGAGCCTGGAACGGAG
 GCTTCTCTGGAACCTGGAAGGAGAAGGCTTCATCCTTGGGGAGTTTTCGTGGTGGGATCA
 GGAAAGCAGGGCATTCTTCTTGAGACCGAGAAAAAGAAATTGGAGACAAAGTAAACCTACT
 TTCTGTTCTGGAAGCTGCTAAGATGATCAAACACAGACTTTGGCCTCAGAAAAAAAT**GA**T
 TGTGTGAAACTGCCAGCTCAGGGATAACCAGGGACATTACCTGTGTTCATGGGATGTATT
 GTTTCACACTCGTGTCCCTAAGGAGTGAGAAACCCATTTATACTCTACTCTCAGTATGGATTA
 TTAATGTATTTTAAATATTCTGTTTAGGCCACTAAGGCAAAATAGCCCCAAAAACAAGACTGA
 CAAAAATCTGAAAAACTAATGAGGATTATTAAGCTAAAACCTGGGAAATAGGAGGCTTAAAA
 TTGACTGCCAGGCTGGGTGCAGTGGCTCACACCTGTAATCCAGCACTTTGGGAGGCCAAGG
 TGAGCAAGTCACTTGAGGTCGGGAGTTCGAGACCAGCCTGAGCAACATGGCGAAACCCGCTC
 TCTACTAAAAATACAAAAATCACCCGGGTGTGGTGGCAGGCACCTGTAGTCCCAGCTACCCG
 GGAGGCTGAGGCAGGAGAATCACTTGAACCTGGGAGGTGGAGGTTGCGGTGAGCTGAGATCA
 CACCCTGTATTCCAGCCTGGGTGACTGAGACTCTAACTAA

FIGURE 268

MSFLQDPSFFTGMWSIGAGALGAAALALLANTDVFLSKPQKALEYLEDIDLKTLKEPR
TFKAKELWEKNGAVIMAVRRPGCFLCREEAADLSSLKSMLDQLGVPLYAVVKEHIRTEVKDF
QPYFKGEIFLDEKKKFYGPQRRKMMFMGFIRLGVWYNFFRAWNGGFSGNLEGEFILGGVFV
VGSGKQGILLEHREKEFGDKVNLLSVLEAAKMIKPQTLASEKK

FIGURE 269

ACGGACCGAGGGTTCGAGGGAGGGACACGGACCAGGAACCTGAGCTAGGTCAAAGACGCCCC
 GGCCAGGTGCCCCGTCGCAGGTGCCCCTGCCCGGAGATGCGGTAGGAGGGGCGAGCGCGAGA
 AGCCCCCTTCCTCGGCGCTGCCAACCCGCCACCCAGCCC**ATG**GCGAACCCCGGGCTGGGGCTG
 CTTCTGGCGCTGGGCCTGCCGTTCTGTGCTGGCCCGCTGGGGCCGAGCCTGGGGGCAAATACA
 GACCACTTCTGCAAATGAGAATAGCACTGTTTTGCCTTCATCCACGCTCCAGCTCCGATG
 GCAACCTGCGTCCGGAAGCCATCACTGCTATCATCGTGGTCTTCTCCCTCTTGGCTGCCTTG
 CTCTGGCTGTGGGGCTGGCACTGTTGGTGCGGAAGCTTCGGGAGAAGCGGCAGACGGAGGG
 CACCTACCGGCCAGTAGCGAGGAGCAGTTCTCCCATGCAGCCGAGGCCCGGGCCCCCTCAGG
 ACTCCAAGGAGACGGTGCAGGGCTGCCTGCCCATC**TAG**GTCCCCTCTCCTGCATCTGTCTCC
 CTTCAATTGCTGTGTGACCTTGGGGAAAGGCAGTGCCCTCTCTGGGCAGTCAGATCCACCCAG
 TGCTTAATAGCAGGGAAGAAGGTACTTCAAAGACTCTGCCCTGAGGTCAAGAGAGGATGGG
 GCTATTCACTTTTATATATTTATATAAAATTAGTAGTGAGATGTAAAAAAAAAAAAAAAAAA

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270/330

FIGURE 270

MANPGLGLLLALGLPELLARWGRAWGQIQTTSANENSTVLPSTSSSSDGNLRPEAITAIIV
VFSLLAALLLAVGLALLVRKLREKRQTEGTYRPSSEEQFSHAAEARAPQDSKETVQGCLPI

101112131415161718192021222324252627282930313233343536373839404142434445464748495051525354555657585960616263646566676869707172737475767778798081828384858687888990919293949596979899100

FIGURE 271

AATATATCATCTATTTATCATTAATCAATAATGTATTCTTTTATTCCAATAACATTTGGGTT
TTGGGATTTTAATTTTCAAACACAGCAGAATGACATTTTCTGTCACTATTATTATTGTTG
GTATGTGAAGCTATTTGGAGATCCAATTCAAGGAAGCAACACATTGGAGAATGGCTACTTCT
ATCAAGAAATAAAGAGAACCACAGTCAACCCACACAATCATCTTTAGAAGACAGTGTGACTC
CTACCAAAGCTGTCAAACCACAGGCAAGGGCATAGTTAAAGGACGGAATCTTGACTCAAGA
GGGTTAATTCTTGGTGCTGAAGCCTGGGGCAGGGGTGTAAAGAAAAACACTTAGATTCAATG
ATTGTAAATTTAAGGCAAATACACATATTAGTATTACCTTAGTGTAATGTATCCCTGTCATA
TATACAATAAGGTGAAATTATAAGTACCCTATGCAGTTGGCTGGACAGTTCTAAATTGGACT
TTATTAATTTTTAAAATCAGTAACTGATTTATCACTGGCTATGTGCTTAGATCTACAGGAGA
TCATATAATTTGATACAAATAAAAGAAAAGTGTTCTCTCCCTTACAGAATTGACATTTTAA
ATGCGATACAGTTAGAATAGGAAATATGACATTAGAAAGGAAGAATGACAGGGAGAAAGGAA
AGAAGGGAAAATGTTGCCAAGGAAAAAAAAA

FIGURE 272

MTFFLSLLLLLVCEAIWRSNSGSNTLENGYFLSRNKENHSQPTQSSLEDSVTPTKAVKTTGK
GIVKGRNLDSRGLILGAEAWGRGVKKNT

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FIGURE 273

GCCAGGAATAACTAGAGAGGAACAA**ATG**GGGTATTTCAGAGGTTTGTGTTTCTCTTAGTTCT
 GTGCCTGCTGCACCACTCAAACTACTTCTTCATTAAAGCTGAATTAATATGGCTTTGAAGATA
 TTGTCATTTGTTATAGATCTAGTGTGCCAGAAGATGAAAAAATAATTGAACAAATAGAGGAT
 ATGGTGACTACAGCTTCTACGTACTGTTTGAAGCCACAGAAAAAGATTTTTTTCAAAAA
 TGTATCTATATTAATTCCTGAGAATTGGACAGGAAAACTCTCAGTACAAAAGGCCAAAACATG
 AAAACCATAAACATGCTGATGTTATAGTTGCGACACCTACACATCCAGGATAGAGATGAACCA
 TACACCAAGCAGTTTCACAGAATGTGGAGAGAAAAGCGCAATACATTACTTACCCCTGACCT
 TCTACTTGGAAAAAACAATAATGAATATGGACCAAGCAGCAAACTGTTTGTCCATGAGTGGG
 CTCACCTCCGGTGGGGAGTGTGTTGATGAGTACAATGAAGATCAGCCTTTCTACCGTGCCTAAG
 TCAAAAAAAATCGAACCAACAAGGTGTTCCCGAGGTATCTCTGTAGAAAATAGAGTTTATAA
 GTGTCAAGGAGGCGAGCTGTCTTAGTAGAGCATGCAAGATTGATTTCAACCAAAACTGTATG
 GAAAAGATTGTCAATTCTTTCTCGATAAAGTACAAACAGAAAAGCATCCATAATGTTTATG
 CAAAGTATTGATTTCTGTTGTTGATTTTGTAAACGAAAAAGCCATTAATCAAGAAGCTCCAAG
 CCTACAAAAAATAAAGTGCRAATTTTGAAGATACATGGGAGGTGATTAGCAATTCTGAGGATT
 TTAATAAACACCATACCCATGGTGACACCACTCTCCACCTGTCTCTCATGGCTGAAGATC
 AGTCAAAAGAAATTTGTGTGCTTGAATTTCTCAATAAGTCTGGAAGCATGGGGGGTAAAGACCCCT
 AAATCGAATGAATCAAGCAGCAAAACATTTCTGCTGCAGACITGTTGAAAATGGATCCTGGG
 TGGGGATGGTTTCACTTTGATAGTACCTGCCACTTCTGTAATAAGCTATCCAAATAAAAAGC
 AGTGATGAAAGAAACACACTGATGCGAGGATTAACATCATATCTCTGGGAGGAATCCCAT
 CTGCTCTGGAATTAATATGCATTTCAAGTGATTTGGAGAGCTACATTTCCCACTCGATGGAT
 CCGAAGTACTGCTGCTGACTGTGATGGGGAGGATAACACTGCAAGTTCTGTATTGATGAAGT
 ACACAAGTGGGGCCATTTGTTCAATTTTATGCTTTTGGGAAGAGCTGCTGATGAAGCAGTAAT
 AGAGTAGAGCAGATGAACAGGAGGAAGTCATTTTATGTTTTCAGATGAAGCTCAGAACATG
 GCCTCATTTGATGCTTTTGGGGCTCTTACATCAGGAAATACTGATCTCTCCGCAAGTGCCTCT
 CAGCTCGAAAGTAAAGGATTAACATGAATAGTAATGCTGAGTGAACGCACTGTCATAAT
 TGATAGTACAGTGGGAAAGGACACGTTCTTCTCATACATGAAGACAGTCTGCTCTCCGATA
 TTTCTCTCTGGGATCCAGTGGAAACATAATGGAATAATTTCAAGCATATACAGAAAATGGCAGATAT
 ATGGCCATCTCAGTATTCAGGAACTGCAAAAGGTGGGCACTGGGCAATCAAACTTCTCAAGC
 CAAAGCAACCCAGAAAACATTAACATTAACGTAACCTCTCGAGCAGCAAAATTTCTTGTGCT
 CTCCAAATCAGATGAATGCTAAAAATGAATAAGGACGTAACAGTTTCCCGAGCCCAATGATT
 GTTTACGCAGAAATTTCTACAGGATATGTACCTGTCTTGGAGCAATGTGACTGCTTTTCAT
 TGAATCAGAGAATGGACATACAGAAGTTTGGAACTTTTGGATTAATGGTGCAGGCGCTGATT
 CTTTCAAGAATGATGGAGTCTACTCCAGGTATTTTACAGCATATACAGAAAATGGCAGATAT
 AGCTTAAAAAGTTCTGGGCTCATGGAGGAGCAACACTGCCAGGCTAAAAATACGGCTCCACT
 GAATAGAGCCGCTACATACCAGGCTGGGTAGTGAACGGGGAATTTGAAGCAAAATCGGCCAA
 GACCTGAATTTGATGAGGATACTCAGACCACCTTGGAGGATTTCAAGCGAAGCAGATCCGGA
 GGTGCAATTTTGGTATTCACAACTCCCAAGCCTTCCCTTGCTGACCAATACCCCAAGTCA
 AATCAGACAGCTTTGATGCCACAGTTTCATGAGGATAAGATTATTTCTTACATGGACAGCAGCAG
 GAGATAATTTTGAATTTGAAAAGTTCAACGTTATATCAAGAAATAGTGCAAGTATTTCTT
 GATCTTAAGAGCAGTTTTGATGATGCTCTCAAGTAAATACTACTGATCTGTCAACAAAGGA
 GGCCAACTCCAAGGAAAGCTTTTGATTTTAAACCAGAAAATCTCAGAGAAAATGCAACCC
 ACATATTTTATGCAATTAAGAGTATAGATAAAAGCAATTTGACATCAAAAGTATCCAACTT
 GCACAAGTAACTTTGTTTATTTCCCTCAAGCAAACTCTGATGACATTGATCCTTACACTCTC
 TACTCTACTCTCTCTCTGATAAAAGTCATAATTTCTGGAGTTAATATTTTACCTGCTGTAT
 TGTCTGTGATGGGCTGTTGTGAATTTGTTAACTTTATTTTAAGTACCACTATTT**GA**CACTT
 ACGAAGAAAAAATCTTCAAGTAGACCTAGAAGAGAGTTTAAAGAAACAAACCAATGTAGT
 AAAGGATATTTCTGAATCTTAAATATCATCCATGTGTGATATAAACTCATAAAAATTAAT
 TTAAGATGTCCGAAAAGGATACTTTGATTAAATAAAACACTCATGGATATGTAAAAACTGT
 CAAGATTAATAATTTAATGATTTTCAATTTATTTTATTTTGAAGAAATAGTGAATGAAC
 AAAGATCTCTTTTCTACTGATACCTGGTTGTATATTTATTTGATGCAACAGTTTTCTGAAT
 GATATTTCAAATTCATCAGAAAATAAAATCATCTATCTGAGTAGTCAAAATGCAAGTAA
 GGAGAGCAAAATAACAACTTTTGGAAAAAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
 AA

FIGURE 274

MGLFRGFVFLVLCLLHQSNSTSFIKLNNNGFEDIVIVIDFSPVEDEKIIIEQIEDMVTTASTY
 LFEATEKRFFFKNVSILIPENWKENPQYKRPKHENHKHADVIVAPPTLPGRDEPYTKQFTEC
 GKGEYIHFTPDLLLGKKQNEYGPPGKLFVHEWAHLRWGVDFEYNEDQPFYRAKSKKIEATR
 CSAGISGRNRVYKCGGSGCLSRACRIDSTTKLYGKDCQFFPDKVQTEKASIMFMQSIDSVVE
 FCNEKTHNQEAPSLQNIKCNFRSTWEVISNSEDFKNTIPMVTPPPPPVFSLKISQRIVCLV
 LDKSGSMGGKDRLNRMNQAAKHFLQTVENGSWVGMVHFDSTATIVNKLIQIKSSDERNTLM
 AGLPTYPLGGTSICSGIKYAFQVIGELHSQLDGSEVLLLLTDGEDNTASSCIDEVKQSGAIVH
 FIALGRAADEAVIEMSKITGGSHFYVSDEAQNGLIDAFGALTSGNTDLSQKSLQLESKGLT
 LNSNAWMNDTVIIDSTVGKDTFFLITWNSLPSPISLWDPSGTIMENFTVDATSKMAYLSIPG
 TAKVGTWAYNLQAKANPETLTITVTSRAANSSVPPITVNAKMNDVNSFPSPMIVYAEILQG
 YVPVLGANVTAPIESQNGHTEVLELLDNGAGADSFKNQGVYSRYFTAYTENGYSYSLKVRHAG
 GANTARLKLRPPLNRAAYIPGWVNGEIEANPPEIDEIDTQTTLDEFSRTASGGAFVVSQV
 PSLPLPDQYPPSQITDLDTATVHEDKIIILTWTPAGDNFDVGKVQRYIIRISASILDLRDSFDD
 ALQVNTTDLSPKEANSKESFAFKPENISEENATHIFIAIKSIDKSNLTSKVSNIAQVTLFIP
 QANPDDIDPTPTPTPTPTPKSHNSGVNISTLVLSVIGSVVIVNFILSTTI

Signal peptide:

amino acids 1-21

Putative transmembrane domains:

amino acids 284-300, 617-633

Leucine zipper pattern.

amino acids 469-491, 476-498

N-glycosylation site.

amino acids 20-24, 75-79, 340-344, 504-508, 542-546, 588-592,
 628-632, 811-815, 832-836, 837-841, 852-856, 896-900

[illegible]

FIGURE 276

MMVVRGGLLAWISRVVLLVLLCCAISVLYMLACTPKGDEEQLALPRANSPTGKEGYQAVLQ
EWEEQHRNYVSSLKRQIAQLKEELQERSEQLRNGQYQASDAAGLGLDRSPPEKTQADLLAFL
HSQVDKAEVNAGVKLATEYAAPFDSFTLQKVYQLETGLTRHPEEKPVRKDKRDELVEAIES
ALETLNNPAENSPNHRPYTASDFIEGIYRTERDKGTLYELTFKGDHKHEFKRLILFRPFSP
MKVNEKLNMAANTLINVIVPLAKRVDKFRQFMQNFREMCIEQDGRVHLTVVYFGKEEINEVK
GILENTSKAANFRNFTFIQLNGEFSRGKGLDVGARFWKGSNVLLFFCDVDIYFTSEFLNTR
LNTQPGKKVFYFVLFSEQYNPGIYGHHDVPPLEQQLVIKKETGFWRDFGFGMTCQYRSDFI
NIGGFDLDIKGWGGEDVHLYRKYLHSNLIVVRTPVRGLFHLWHEKRCMDELTPQYKMCMS
KAMNEASHGQLGMLVFRHEIEAHLRKQKQKTSKKKT

FIGURE 277

GAAAGAATGTTGTGGCTGCTCTTTTTTCTGGTGACTGCCATTCATGCTGAACTCTGTCAACC
 AGGTGCAGAAAATGCTTTTAAAGTGAAGTATAGTATCAGAACAGCTCTGGGAGATAAAGCAT
 ATGCTCTGGGATACCAATGAAGAATACCTCTTCAAAGCGATGGTAGCTTTCTCCATGAGAAAA
 GTTCCCAACAGAGAAGCAACAGAAATTCCCATGTCTACTTTGCAATGTAACCCAGAGGGT
 ATCATTCTGGTTTGTGGTTACAGACCCCTTCAAAAAATCACACCCCTTCTGCTGTTGAGGTGC
 AATCAGGCATAAGAATGAACAAGAACCGGATCAACAATGCCTTCTTTCTAAATGACCAAAT
 CTGGAATTTTTAAAAATCCCTTCCACACTTGACACCCCATGGACCCATCTGTGCCCATCTG
 GATTATTATATTGGTGTGATATTTTGCATCATCATAGTTGCAATTGCACTACTGATTTTAT
 CAGGGATCTGGCAACGTAGAAGAAAGAAACAAGAACCATCTGAAGTGGATGACGCTGAAGAT
 AAGTGTGAAAACATGATCACAATTGAAAATGGCATCCCTCTGATCCCCTGGACATGAAGGG
 GGGCATATTAAATGATGCCTTCATGACAGAGGATGAGAGGCTCACCCCTCTCTGAAGGGCTGT
 TGTCTGCTTCTCAAGAAATTAAACATTTGTTTCTGTGTGACTGCTGAGCATCTGAAATA
 CCAAGAGCAGATCATATATTTTGTTCACCATTTCTCTTTTGAATAAAATTTGAATGTGCT
 TGAAAGTGAAGCAATCAATTATACCCACCAACACCACTGAAATCATAGCTATTTCACGAC
 TCAAAATATTCTAAAAATTTTTTCTGACAGTATAGTGTATAAATGTGGTCATGTGGTATTTG
 TAGTTATTGATTTAAGCATTTTTAGAAATAAGATCAGGCATATGTATATATTTTCACTTC
 AAAGACCTAAGGAAAAATAAATTTCCAGTGGAGAATACATATAATATGGTGTAGAAATCAT
 TGAAAATGGATCCCTTTTGAAGTCACTTATATCACTCTGTATATGACTAAGTAACAAAAAG
 TGAGAAGTAATTATTGTAAATGGATGGATAAAAAATGGAATTACTCATATACAGGGTGAATT
 TTATCCTGTTATCACACCAACAGTTGATTATATATTTTCTGAATATCAGCCCTAATAGGAC
 AATTCTATTTGTGACCATTCTACAATTTGTAAAGTCCAATCTGTGCTAACTTAATAAAG
 TAATAATCATCTCTTTTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 278

MLWLLFFLVTAIHAELCQPGAENAFKVRLSIRTALGDKAYAWDTNEEYLFKAMVAFSMRKVP
NREATEISHVLLCNVTQRVSFVFWVTDPSKNHTLPAVEVQSAIRMNKNRINNAFFLNDQTLE
FLKIPSTLAPPMDPSVPIWIIIFGVIFCIIIVAIALLILSGIWQRRRKNKEPSEVDDAEDKC
ENMITIENGIPSDPLDMKGGILMMPS

FIGURE 279

AACTCAAACCTCTCTCTCTGGGAAAACGCGGTGCTTGCTCCTCCCGAGTGGCCTTGGCAGG
 GTGTTGGAGCCCTCGGTCTGCCCCGTCCGGTCTCTGGGGCCAAGGCTGGGTTTCCCTC**ATGT**
 ATGGCAAGAGCTCTACTCGTGCGGTGCTTCTTCTCCTTGGCATACAGCTCACAGCTCTTTGG
 CCTATAGCAGCTGTGGAAATTTATACCTCCCGGGTGCTGGAGGCTGTTAATGGGACAGATGC
 TCGGTTAAATGCACTTTCTCCAGCTTTGCCCTGTGGGTGATGCTCTAACAGTGACCTGGA
 ATTTTCGTCTCTAGACGGGGACCTGAGCAGTTTGTATTCTACTACCACATAGATCCCTTC
 CAACCCATGAGTGGGCGGTTTAAGGACCGGGTGTCTTGGGATGGGAATCCTGAGCGGTACGA
 TGCCTCCATCCTTCTCTGGAAACTGCAGTTCGACGACAATGGGACATACACCTGCCAGGTGA
 AGAACCCACCTGATGTTGATGGGGTGATAGGGGAGATCCGGCTCAGCGTCGTGCACACTGTA
 CGCTTCTCTGAGATCCACTTCCTGGCTCTGGCCATTGGCTCTGCCTGTGCACTGATGATCAT
 AATAGTAATTGTAGTGGTCTCTTCCAGCATTACCGGAAAAAGCGATGGGCCGAAAGAGCTC
 ATAAAGTGGTGGAGATAAAATCAAAGAAGAGGAAAGGCTCAACCAAGAGAAAAAGGTCTCT
 GTTTATTTAGAAGACACAGAC**TAA**CAATTTTAGATGGAAGCTGAGATGATTTCCAAGAACA
 GAACCCTAGTATTTCTTGAAGTTAATGGAACTTTTCTTTGGCTTTTCCAGTTGTGACCCGT
 TTTCCAACCAGTTCTGCAGCATATTAGATTCTAGACAAGCAACACCCCTCTGGAGCCAGCAC
 AGTGCTCCTCCATATCACCAGTCATACACAGCCTCATTATTAAGGTCTTATTTAATTCAGA
 GTGTAATTTTTTCAAGTGCTCATTAGGTTTTATAACAAGAAGCTACATTTTTGCCCTTAA
 GACACTACTTACAGTGTTATGACTTGATACACATATATTGGTATCAAAGGGGATAAAGCC
 AATTTGTCTGTTACATTTCTTTTACGTATTTCTTTTACGAGCACTCTGCTACTAAAGTTA
 ATGTGTTTACTCTCTTCTCTCCACATTCTCAATTAAAGGTGAGCTAAGCCTCCTCGGTG
 TTTCTGATTAACAGTAAATCCTAAATCAAAGTGTAAATGACATTTTTATTTTATGTCTC
 TCCTTAACATGAGACACATCTTGTTTACTGAATTTCTTCAATATTCAGGTGATAGATT
 TTTGTCG

FIGURE 280

MYGKSSTRAVLLLLGIQLTALWPAAVEIYTSRVLEAVNGTDARLKCTFSSFAPVGDALTVT
WNFRPLDGGPEQFVFYYHIDPFQPMGRFKDRVSWDGNPERYDASILLWKLQFDDNGTYTCQ
VKNFPDVGVIIEIRLSVVHTVRFSEIHFLALAIGSACALMI IIVVVVLFQHYRKKRWAER
AHKVVEIKSKEEERLNQEKVSVYLEDTD



FIGURE 281

GCATTTTTGTCTGTGCTCCCTGATCTTCAGGTCACCACCATGAAGTTCTTAGCAGTCCTGGT
ACTCTTGGGAGTTTCCATCTTTCTGGTCTCTGCCCAGAATCCGACAACAGCTGCTCCAGCTG
ACACGTATCCAGCTACTGGTCCTGCTGATGATGAAGCCCCTGATGCTGAAACCACTGCTGCT
GCAACCACTGCGACCACTGCTGCTCCTACCACTGCAACCACCGCTGCTTCTACCACTGCTCG
TAAAGACATTCCAGTTTTTACCCAAATGGGTTGGGGATCTCCCGAATGGTAGAGTGTGTCCCTT
GAGATGGAATCAGCTTGAGTCTTCTGCAATTGGTCACAACATATTCATGCTTCCTGTGATTTC
ATCCAACACTTACCTTGCCCTACGATATCCCCTTTATCTCTAATCAGTTTATTTTCTTTCAA
ATAAAAAATAACTATGAGCAACATAAAAAAAAAAAAAA

FIGURE 282

MKFLAVLVLLGVSIFLVSAQNPTTAAPADTYPATGPADDEAPDAETTAAATTATTAAPTTAT
TAASTTARKDIPVLPKWVGDLPNGRVCP

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FIGURE 283

GGACTCTGAAGGTCCCAAGCAGCTGCTGAGGCCCCCAAGGAAGTGGTTCCAACCTTGGACCC
 CTAGGGGTCTGGATTTGCTGGTTAACAGATAACCTGAGGGCAGGACCCCATAGGGGAATGC
 TACCTCCTGCCCTTCCACCTGCCCTGGTGTTCACGGTGGCCTGGTCCCTCCTTGCCGAGAGA
 GTGTCTGGGTCAGGGACGCAGAGGACGCTCACAGACTCCAGCCCTTTGTTACCGAGAGGAC
 ACTTGGCAAGGTCCAGCGATGGTCCGGAGTCCACACACAGACTGGCGGCAGGGCAGGAGGGG
 GACAGTTCTGTTGTGCTTGGTTGGACAGTAAGAGGGTCTTGGCCAGTCCAGGGTGGGGGGCG
 GCAAACTCCATAAAGAACCAGAGGGTCTGGGCCCCGGCCACAGAGTCATCTGCCCAGCTCCT
 CTGCTGCTGGCCAGTGGGAGTGGCACGAGGTGGGGCTTTGTGCCAGTAAAAAACCACAGGCTGG
 ATTTGCCCTGCGGGCCATGGTCCCTGTCTAGGGCAGCAATTCTCAACCTTCTTGCTCTCAGGA
 CCCCAAAGAGCTTTCATTGTATCTATTGATTTTTTACCACATTAGCAATTAAAACTGAGAAAT
 GGGCCGGGCACGGTGGCTCACGCCGTGAATCCAGCACTTTGGGAGGCCGAGGCGGGTGGAT
 CACCTGAGATCAGGAGTTCAAGACCAGCCTGGCCAACATGGTGAAACCTTGCTACTAAAAA
 TACAAAAAATTAGCCAGGCACAGTGGTGTGCACTGGTAGTCCCAGTTACTCGGGAGGCTGAG
 GCAGGAAATCGCTTGAACCCAGGAGCGGACGTTGCGGTGAGCCGAGATCGCGCCGTGAT
 TCCAGCCTGGGCGACAAGAGTGAGACTCCATCTCACACA

FIGURE 284

MLPPALPPALVFTVAWSLLAERVSWVRDAEDAHRIQPFVVERTLGKVQRWSGVHTQTGGRAG
GGQFCCAWLDSKRVLASPGWGAANSIKNQRVWAPATESSAQLLCCWPVGVARGGALCQ

FIGURE 285

GT**CATG**CCAGTGCCTGCTCTGTGCCTGCTCTGGGCCCTGGCAATGGTGACCCGGCCTGCCTCA
 GCGGCCCCCATGGGCGGCCCAGAACTGGCACAGCATGAGGAGCTGACCCCTGCTCTTCCATGG
 GACCCCTGCAGCTGGGCCAGGCCCTCAACGGTGTGTACAGGACCACGGAGGGACGGCTGACAA
 AGGGCAGGAACAGCCCTGGGTCTCTATGGCCGCACAATAGAACTCCTGGGGCAGGAGGTCAGC
 CGGGGCCGGGATGCAGCCAGGAACCTCGGGCAAGCCTGTTGGAGACTCAGATGGAGGAGGA
 TATTCTGCAGCTGCAGGCAGAGGCCACAGCTGAGGTGCTGGGGGAGGTGGCCAGGCACAGA
 AGGTGCTACGGGACAGCGTGCAGCGGCTAGAAGTCCAGCTGAGGAGCGCCTGGCTGGGCCCT
 GCCTACCGAGAATTTGAGGTCTTAAAGGCTCACGCTGACAAGCAGAGCCACATCCTATGGGC
 CCTCACAGGCCACGTGCAGCGGCAGAGGCGGGAGATGGTGGCACAGCAGCATCGGCTGCGAC
 AGATCCAGGAGAGACTCCACACAGCGGCGCTCCAGCC**TGA**ATCTGCCTGGATGGAAGTGA
 GACCAATCATGTGCAAGGAACACTTCCACGCCCCGTGAGGCCCTGTGCAGGGAGGAGCTG
 CCTGTTCCTGGGATCAGCCAGGGCGCCGGGCCCCACTTCTGAGCACAGAGCAGAGACAGAC
 GCAGGCGGGGACAAAGGCAGAGGATGTAGCCCCATTTGGGGAGGGGTGGAGGAAGGACATGTA
 CCTTTTCATGCCACACCCCTCATTAAGCAGAGTCGTGGCATTTCAAAAAAAAAAAAAAAA
 AAAAAAAAAAAAAAAAAAAAAA

FIGURE 286

MPVPALCLLWALAMVTRPASAAPMGGPELAQHEELTLLFHGTLQLGQALNGVYRTTEGRLTK
ARNSLGLYGRTIELLGQEVSRGRDAAQELRASLLETQMEEDILQLQAEATAEVLGEVAQAQK
VLRDSVQRLEVQLRSAWLGPAYREFEVLKAHADKQSHILWALTGHVQRQRREMVAAQQHRLRQ
IQERLHTAALPA

FIGURE 287

GGCAAC**ATG**GCTCAGCAGGCTTGCCCCAGAGCCATGGCAAAGAATGGACTTGTAAATTTGCAT
 CCTGGTGATCACCTTACTCCTGGACCAGACCACCAGCCACACATCCAGATTAAAAGCCAGGA
 AGCACAGCAAACGTCGAGTGAGAGACAAGGATGGAGATCTGAAGACTCAAATTTGAAAAGCTC
 TGGACAGAAGTCAATGCCTTGAAGGAAATTCAGGCCCTGCAGACAGTCTGTCTCCGAGGCAC
 TAAAGTTTACAAGAAATGTACCTTGCTTCAGAAGGTTTGAAGCATTTCCATGAGGCCAATG
 AAGACTGCATTTCCAAAGGAGGAATCCTGGTTATCCCCAGGAACCTCCGACGAAATCAACGCC
 CTCCAAGACTATGGTAAAAGGAGCCTGCCAGGTGTCAATGACTTTTGGCTGGGCATCAATGA
 CATGGTCACGGAAGGCAAGTTTGTGACGTCAACGGAATCGCTATCTCCTTCTCAACTGGG
 ACCGTGCACAGCCTAACGGTGGCAAGCGAGAAAACCTGTGTCTTCTCCCAATCAGCTCAG
 GGCAAGTGGAGTGATGAGGCCTGTGCGAGCAGCAAGAGATACATATGCGAGTTCACCATCCC
 TAA**ATAG**TGCTTTTCTCCAATGTGTCTCCAAGCAAGATTATCATATACTTATAGGTTTCATGA
 TCTCTAAGATCAAGTAAAAATCATAATTTTTACTTATTAATAAATGCAACACAAGATCAAT
 GTCCATAGCAATATGATAGCATCAGCCAATTTTGTAACACATTTCTTTGGGATTTTGCCCT
 TCCTGGGGTATAGGGGATCAGAAATATTGATCCATGTGCACGCAGATAAAATGGCTTCTGTCT
 AAACAGACTAAAATCTTTCTCTCTAGTCTTTCTCACTTGTAACAAACCAAGTTTGTTTTCAA
 AAATCACAGTAGCAATGCAACTCATCACTCTAGAAAAGCAAGCTTAGGCTACCTGAAAGATT
 TTCCTTGGGAAGTTTAGCGTATGTTGACTAACAAAAATTCCTACATCAGAGACTCTAGGT
 GCTATATAATCCAAAACTTTTCAGCCTGTTGCTCATTCTGTCCCATGCTGGCAATAATACC
 TTGTGAGCCCATTACCCTTATTTTGAATTGCTCCATCTCCTGGTGGGACTTGTATCTTGTCT
 GCCATATCAGAACACAAACCCCTGAAGAGGTTCTGATTTGATTTTTTTTTTTTCTTCATGCC
 TACCCTTTTTTTGGAAGTTTCCAGCCGCAATTTGAAATGAAATGACAAGGTGTATATTGAT
 CAATTTTCATTCCCACCATTGCATTACAACCTCTAACTTAAATGGGTAAACCTAAGGCATAT
 CAAAGAAGCAGATTGCATGATAAACGGAATAGAAAAAAGAACCTACATTTATTTTGCTTT
 AGCATCCTTACTCTCACCTTTTATGAGATTGAGAGTGGAATTTACATTTCTTTTACATTT
 TCGTATATTTATTTTTTTAGCCATCATTATATGTTTAACTCTATTATGGGCAACCAATCTT
 TGGGAAGCTGAAAACCTGAATTTAAAGAATGCTATCTTGGAAAATTCATACGCTCTGTGCAATT
 TTTTATTCGCTAGTGCTATTCTGCTTGTGTTAACTAGATTGTACAAAATAAATTCATTGCT
 TAATATCAAATACAAAGTTTAGACTTGAGGGAAATGGGCTTTTTAGAACAAACAATTTT
 AAATATATTTTGTCTTCAATAAATAGTGTTTAAACATTGAATGTGTTTTGTGAACAATAT
 CCCACTTTGCAAACTTTAACTACACATGCTTGAATTAAGTTTTAGCTGTTTTCTATGCTCA
 ATAATAAGCCTGAATCTGATCAATAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 288

MAQQACPRAMAKNGLVICILVITLLLDQTTSHTSRLKARKHSKRRVRDKDGD LKTQIEKLWT
EVNALKEIQALQTVCLRGTKVHKKCYLASEGLKHFHEANEDCISKGGILVIPRNSDEINALQ
DYGKRSLPGVNDFWLGINDMVTEGKFVDVNGIAISFLNWDRAQPNGGKRENCVLFSQSAQGK
WSDEACRSSKRYICEFTIPK

FIGURE 289

GCGAGGACCGGGTATAAGAAGCCTCGTGGCCTTGCCCGGGCAGCCGCAGGTTCCCCGCGCGC
CCCGAGCCCCCGCGCCATGAAGCTCGCCGCCCTCCTGGGGCTCTGCGTGGCCCTGTCTCTGCA
GCTCCGCTGCTGCTTTCTTAGTGGGCTCGGCCAAGCCTGTGGCCAGCCTGTCGCTGCGCTG
GAGTCGGCGGGCGAGGCCGGGGCCGGGACCCTGGCCAACCCCTCGGCACCCCTCAACCCGCT
GAAGCTCCTGCTGAGCAGCCTGGGCATCCCCGTGAACCACCTCATAGAGGGCTCCAGAAAGT
GTGTGGCTGAGCTGGGTCCCCAGGCCGTGGGGGCCGTGAAGGCCCTGAAGGCCCTGCTGGGG
GCCCTGACAGTGTTTGGCTTGAGCCGAGACTGGAGCATCTACACCTGAGGACAAGACGCTGCC
CACCCGCGAGGGCTGAAAACCCCGCCGCGGGGAGGACCGTCCATCCCCTTCCCCCGGCCCTT
CTCAATAAACGTGGTTAAGAGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAA

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FIGURE 290

MKLAALLGLCVALSCSSAAAFVGS AKPV AQPVAALESAAEAGAGTLANPLGTLNPLKLLLS
SLGIPVNHIEGSQKCV AELGPQAVGAVKALKALLGALT VFG

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FIGURE 291

TGAAGGACTTTTCCAGGACCCAAGGCCACACACTGGAAGTCTTGACAGTGAAGGGAGGCAC
 CCTTGGCCTCCGACGCGCATCACATGAAGGTGGTGCCAAAGTCTCCTGCTCTCCGTCCTCCTG
 GCACAGTGTGGCTGGTACCCGGCTTGGCCCCAGTCTCAGTCGCCAGAGACCCAGCCCC
 TCAGAACCAGACCAGCAGGGTAGTGCAGGCTCCAGGGAGGAAGAGGAGATGAGCAGGAGG
 CCAGCGAGGAGAAGGCCGGTGAGGAAGAGAAAGCCTGGCTGATGGCCAGCAGGCAGCAGCTT
 GCCAAGGAGACTTCAAACCTTCGATTGAGCCTGCTGCGAAAGATCTCCATGAGGCACGATGG
 CAACATGGTCTTCTCCTCCATTTGGCATGTCTTGGCCATGACAGGCTTGATGCTGGGGGCCA
 CAGGGCCGACTGAAACCCAGATCAAGAGAGGGCTCCACTTGCAGGCCCTGAAGCCCAACAAG
 CCCGGGCTCCTGCCTTCCCTCTTTAAGGGACTCAGAGAGACCTCTCCCGCAACCTGGAAC
 GGGCCTCTCAGAGGGGAGTTTTGCCTTCATCCACAAGGATTTTGATGTCAAAGAGACTTCT
 TCAATTTATCCAAGAGGTATTTTGATACAGAGTGCCTGCTATGAATTTTCGCAATGCCTCA
 CAGGCCAAAAGGCTCATGAATCATTACATTAACAAGAGACTCGGGGGAAAATTTCCCAAAC
 GTTTGATGAGATTAATCCTGAAACCAATTAATTCTTGTGGATTACATCTTGTTCAAAGGGA
 AATGGTTGACCCCATTTGACCCGTGTCTTCAACGAAGTCGACACTTTCCACCTGGACAAGTAC
 AAGACCATTAAGGTGCCCATGATGTACGGTGCAGGCAAGTTTGCCTCCACCTTTGACAAGAA
 TTTTCGTGTGCATGTCCTCAAACCTGCCCTACCAAGGAAATGCCACCATGCTGGTGGTCTCA
 TGGAGAAAATGGGTGACCACCTCGCCCTTGAAGACTACCTGACCACAGACTTGGTGGAGACA
 TGGCTCAGAAACATGAAAACAGAAACATGGAAAGTTTCTTTCCGAAGTTCAGCTAGATCA
 GAAGTATGAGATGCATGAGCTGCTTAGGCAGATGGGAATCAGAGAATCTTCTCACCCCTTG
 CTGACCTTAGTGAACCTCTCAGCTACTGGAAGAAATCTCCAAGTATCCAGGGTTTTACGAAGA
 ACAGTGATTGAAGTTGATGAAAGGGGCACTGAGGCAGTGGCAGGAATCTTGTCAAGAAATAC
 TGCTTATTCATGCCTCCTGTGCATCAAAGTGGACCGGCCATTTCAATTCATGATCTATGAAG
 AAACCTCTGGAATGCTTCTGTTTCTGGGCAGGGTGGTGAATCCGACTCTCCTATTAATTCAGG
 ACATGCATAAGCACTTCGTGCTGTAGTAGATGCTGAATCTGAGGTATCAACACACACAGGA
 TACCAGCAATGGATGGCAGGGGAGAGTGTTCTTTTGTCTTAACTAGTTTAGGGTGTTCTC
 AAATAAATACAGTAGTCCCACCTATCTGAGGGGGATACATTCAAAGACCCCCAGCAGATGC
 CTGAAACGGTGGACAGTGTGAACCTTATATATATTTTTTCTACACATACATACCTATGAT
 AAAGTTTAAATTTATAAATTAGGCACAGTAAGAGATTAACAATAAACAACATTAAGTAAAA
 TGAGTTACTTGAACGCAAGCACTGCAATACCATAACAGTCAAACCTGATTATAGAGAAGGCTA
 CTAAGTGACTCATGGGCGAGGAGCATAGACAGTGTGGAGACATTTGGCAAGGGGAGAATTCA
 CATCCTGGGTGGGACAGACGAGCAGCATGCAAGATTCATCCCACTACTCAGAATGGGATGC
 TGCTTAAGCACTTTTAGATGTGTTATTCTGGAATTTTTTCATTTAAGTGTGTTTGGACCATGGT
 TGACCATGGTTAACTGAGCTCAGAAAGCAAAACCATGGATAAGGGAGGACTACTACAAAA
 GCATTAAATTGATACATATTTTTTAAAAA

FIGURE 292

MKVVPSLLLSVLLAQVWLVPLAPSPQSPETPAPQNQTSRVVQAPREEEDEQEASEEKAGE
EEKAWLMASRQQLAKETSNFGFSLLRKISMHDGNMVFSFPGMSLAMTGLMLGATGPTETQI
KRGLHLQALKPTKPGLLPSLFKGLRETLNRNLELGLSQGSFAFIHKDFDVKETFFNLSKRYF
DTECVPMNFRNASQAKRLMNHYINKETRGKIPKLFDEINPETKLILVDYILFKGKWLTPFDP
VFTEVDTFHLDKYKTIKVPMMYGAGKFASTFDKNFRCHVLKLPYQGNATMLVVLMEKMGDHL
ALEDYLTDLVETWLRNMKTRNMEVFFPKFKLDQKYEMHELLRQMGIRRIFFSPFADLSELSA
TGRNLQVSRVLRRTVIEVDERGTEAVAGILSEITAYSMPPVIKVDRPFHFMIYEETSGMLLF
LGRVVNPTLL

FIGURE 293

CTGGGATCAGCCACTGCAGCTCCCTGAGCACTCTCTACAGAGACGCGGACCCAGACATGAG
GAGGCTCCTCCTGGTCACCAGCCTGGTGGTTGTGCTGCTGTGGGAGGCAGGTGCAGTCCCAG
CACCCAAGGTCCCTATCAAGATGCAAGTCAAACACTGGCCCTCAGAGCAGGACCCAGAGAAG
GCCTGGGGCGCCCGTGTGGTGGAGCCTCCGGAGAAGGACGACCAGCTGGTGGTGTCTGTTCCC
TGTCCAGAAGCCGAAACTCTTGACCACCGAGGAGAAGCCACGAGGTGAGGGCAGGGGCCCA
TCCTTCCAGGCACCAAGGCCTGGATGGAGACCAGGACACCCCTGGGCCGTGTCTGAGTCCC
GAGCCCGACCATGACAGCCTGTACCACCCCTCCGCCTGAGGAGGACAGGGCGAGGAGAGGCC
CCGGTTGTGGGTGATGCCAAATCACCAGGTGCTCCTGGGACCGGAGGAAGACCAAGACCACA
TCTACCACCCCAGTAGGGCTCCAGGGGCCATCACTGCCCCGCCCTGTCCCAAGGCCAGG
CTGTTGGGACTGGGACCCTCCCTACCCTGCCCCAGCTAGACAAATAAACCCAGCAGGCAAA
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FIGURE 294

MRRLLLVTSLVVVLLWEAGAVPAPKVP IKMQVKHWPSEQDPEKAWGARVVEPPEKDDQLVVL
FPVQKPKLLTTEEKPRGQGRGPILPGTKAWMETEDTLGRVLSPEPDHDSLYHPPPEEDQGEE
RPRLWVMPNHQVLLGFEEEDQDHIYHPQ



FIGURE 295

AGAAAGCTGCACTCTGTTGAGCTCCAGGCGCAGTGGAGGGAGGGAGTGAAGGAGCTCTCTG
 TACCCAAGGAAAGTGCACTGAGACTCAGACAAGATTACAATGAACCAACTCAGCTTCTCTGC
 TGTTCCTCATAGCGACCACAGAGGATGGAGTACAGATGAGGCTAATACTTACTTCAAGGAA
 TGGACCTGTTCTTCGTCTCCATCTCTGCCAGAAGCTGCAAGGAAATCAAAGACGAATGTCC
 TAGTGACATTTGATGGCCTGTATTTTCTCCGCACTGAGAATGGTGTTATCTACCAGACCTTCT
 GTGACATGACCTCTGGGGGTGGCGGCTGGACCCTGGTGGCCAGCGTGCATGAGAATGACATG
 CGTGGGAAGTGACGGTGGGCGATCGCTGGTCCAGTCAGCAGGGCAGCAAAGCAGACTACCC
 AGAGGGGGACGGCAACTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCG
 ATGACTACAAGAACCCTGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCACGTG
 CCCAATAAGTCCCCCATGCAGCACTGGAGAAACAGCTCCCTGCTGAGGTACCGCACGGACAC
 TGGCTTCCTCCAGCACTGGGACATAATCTGTTTGGCATCTACCAGAAATATCCAGTGAAT
 ATGGAGAAGGAAAGTGTGGACTGACAACGGCCCGGTGATCCCTGTGGTCTATGATTTTGGC
 GACGCCAGAAACAGCATCTTATTACTACCCCTATGGCCAGCGGGGAATTAAGTGGGGATT
 TGTTCACTTCAGGGTATTTAATAACGAGAGAGCAGCCAACGCCTTGTGTCTGGAATGAGGG
 TCACCGGATGTAACACTGAGCATCACTGCATTGGTGGAGGAGGATACTTCCAGAGGCCAGT
 CCCAGCAGTGTGGAGATTTTCTGGTTTGGATTGGAGTGATATGGAATCATGTTGGTTA
 CAGCAGCAGCCGTGAGATAACTGAGGCAGCTGTGCTTCTATTCTATCGTTGAGAGTTTTGTG
 GGAGGGAACCCAGACCTCTCCTCCCAACCATGAGATCCCAAGGATGGAGAACAACTTACCCA
 GTAGCTAGAATGTTAATGGCAGAAGAGAAAAACAATAATCATATTGACTCAAGAAAAAAA

FIGURE 296

MNQLSFLLFLIATTRGWSTDEANTYFKEWTCSSSPSLPRSCKEIKDECPSAFDGLYFLRTEN
 GVIYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDWSSQQGSKADYPEGDGNWANYNTFG
 SAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSSLLRYRTDTGFLQTLGHNLFGI
 YQKYPVKYGEKGCWTDNGPVI PVVYDFGDAQKTASYSPYGGQREFTAGFVQFRVFNNERAAN
 ALCAGMRVTGCNTEHHCIGGGGYFPEASPPQCGDFSGFDWSGYGTHVGYSRSREITEAAVLL
 FYR

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FIGURE 297

GCGGAGCGGCGCGCGCTGCGCAGAGGAGCCGCTCTCGCCGCCGCCACCTCGGCTGGGAGCC
 CACGAGGCTGCCGCATCCTGCCCTCGGAACAATGAGGACTCGGCGCGGAGGTGCTTGGGCCG
 CGCTGCTCCTGGGGACGCTGCAGGTGCTAGCGCTGCTGGGGGCCGCCATGAAAGCGCAGCC
 ATGGCGGCATCTGCAACATAGAGAATTCTGGGCTTCCACACAACTCCAGTGCTAACTCAAC
 AGAGACTCTCCAACATGTGCCTTCTGACCATACAAATGAAACTTCCAACAGTACTGTGAAAC
 CACCAACTTCAGTTGCCTCAGACTCCAGTAATACAACGGTCACCACCATGAAACCTACAGCG
 GCATCTAATACAACAACACCAGGGATGGTCTCAACAAATATGACTTCTACCACCTTAAAGTC
 TACACCCAAAACAACAAGTGTTCACAGAACACATCTCAGATATCAACATCCACAATGACCG
 TAACCCACAATAGTTCAGTGACATCTGCTGCTTCATCAGTAACAATCACACAACATATGCAT
 TCTGAAGCAAAGAAAGGATCAAAATTTGATACTGGGAGCTTTGTTGGTGGTATTGTATTAAC
 GCTGGGAGTTTATCTATTCTTTACATTGGATGCAAAATGTATTACTCAAGAAGAGGCATTC
 GGTATCGAACCATAGATGAACATGATGCCATCATTAAAGGAAATCCATGGACCAAGGATGGA
 ATACAGATTGATGCTGCCCTATCAATTAATTTTGGTTTATTAATAGTTTAAACAATATTTCT
 CTTTTTGGAAATAGTATAAACAGGCCATGCATATAATGTACAGTGTATTACGTAAATATGTA
 AAGATTCTTCAAGGTAACAAGGGTTTGGGTTTGAATAAACATCTGGATCTTATAGACCGT
 TCATACAATGGTTTTAGCAAGTTCATAGTAAGACAACAAGTCCTATCTTTTTTTTTTGGCT
 GGGGTGGGGCATTGGTCACATATGACCAGTAATTGAAAGACGTCACTACTGAAAGACAGAA
 TGCCATCTGGGCATACAAATAAGAAGTTTGTACAGCACTCAGGATTTGGGTATCTTTTGT
 AGCTCACATAAAGAACTTCAGTGCTTTTCAGAGCTGGATATATCTTAATTACTAATGCCACA
 CAGAAATTATACAATCAAACATAGATCTGAAGCATAAATTAAGAAAAACATCAACATTTTTTG
 TGCTTTAACTGTAGTAGTTGGTCTAGAAACAAAATACTCC

FIGURE 298

MGLGARGAWAALLLGLQLQVLALLGAAHESAAMAASANIENSGLPHNSSANSTETLQHVPSDH
TNETSNSTVKPPTSVASDSSNTTVITMKPTAASNTTTPGMVSTNMTSTTLKSTPKTTSVSQN
TSQISTSTMVTHNSSVTSAASSVTITTTMHSEAKKGSKFDTGSFVGGIVLTLGVLSILYIG
CKMYYSRRGIRYRTIDEHDAII



FIGURE 299

CAGCCGGGTCCCAAGCCTGTGCCTGAGCCTGAGCCTGAGCCTGAGCCCCAGCCGGGAGCCGG
 TCGCGGGGGCTCCGGGCTGTGGGACCGCTGGGCCCCAGCGATGCGCGACCCTGTGGGAGGC
 CTTCTTCGGCTTGGCTCCTTGCTCAGCCTGTGCTGCTGGCGCTTCCGTGCTGCTGCTGGC
 GCAGCTGTGAGACGCCGCCAAGAAATTCGAGGATGTCAGATGTAAATGTATCTGCCCTCCCT
 ATAAAGAAAATTCGGGCATATTTATAATAAGAACATATCTCAGAAAGATTGTGATTGCCTT
 CATGTTGTGGAGCCCATGCCTGTGCGGGGGCCTGATGTAGAAGCATACTGTCTACGCTGTGA
 ATGCAAATATGAAGAAAGAAGCTCTGTCACAATCAAGGTTACCATTATAATTTATCTCTCCA
 TTTTGGGCCTTCTACTTCTGTACATGGTATATCTTACTCTGGTTGAGCCCATACTGAAGAGG
 CGCCTCTTTGGACATGCACAGTTGATACAGAGTGATGATGATATTGGGGATCACCAGCCTTT
 TGCAAATGCACACGATGTGCTAGCCCGCTCCCGCAGTCGAGCCAACGTGCTGAACAAGGTAG
 AATATGCACAGCAGCGTGGAAAGCTTCAAGTCCAAGAGCAGCGAAAGTCTGCTTTGACCGG
 CATGTTGTCTCAGCTAAATTGGGAATTGAATCAAGGTGACTAGAAAGAAACAGGCAGACAA
 CTGGAAGAACTGACTGGGTTTTGCTGGGTTTCATTTTAATACCTTGTGATTTCACCAACT
 GTTGCTGGAAGATTCAAACTGGAAGCAAAAACCTTGCTTGATTTTTTTTTCTTGTTAACGTA
 ATAATAGAGACATTTTTAAAGCACACAGCTCAAAGTCAGCCAATAAGTCTTTTCCTATTTG
 TGACTTTTACTAATAAAAAATAAATCTGCCTGTAAATTATCTTGAAGTCCTTTACCTGGAACA
 AGCACTCTCTTTTACCACATAGTTTTAACTTGACTTTCAAGATAATTTTCAGGGTTTTTG
 TTGTTGTTGTTTTTTGTTTGTGTTTTGTTGGTGGGAGGGGAGGGATGCCTGGGAAGTGTT
 AACAACTTTTTCAAGTCACTTTACTAAACAAACTTTTGTAATAGACCTTACCTTCTATTT
 TCGAGTTTCATTTATATTTTGCAGTGTAGCCAGCCTCATCAAAGAGCTGACTTACTCATTTG
 ACTTTTGCACTGACTGTATTATCTGGGTATCTGCTGTGCTGCACTTCATGGTAAACGGGAT
 CTAATGCACTCCTAGAACAACTGGCCATTGCTAGTTTACTCTAAGACTAAACATAGTCTTG
 GTGTGTGTGGTCTTACTCATCTTCTAGTACCTTTAAGGACAAATCCTAAGGACTTGGACACT
 TGCAATAAAGAAATTTTATTTTAAACCAAGCCTCCCTGGATTGATAATATATACACATTTG
 TCAGCATTTCCGGTCGTGGTGAGAGGCAGCTGTTGAGCTCCAATATGTGCAGCTTTGAACT
 AGGGCTGGGGTGTGGGTGCCTCTTCTGAAAGGTCTAACCATTATTGGATAAAGGCTTTT
 TCTTCCTATGTCTCTTTGGAATGTAAACAATAAAAATAATTTTTGAAACATCAA

300/330

FIGURE 300

MATLWGGLRLGSLLSLCLALSVLLLAQLSDAAKNFEDVRCKCICPPYKENS
GHYKNIS QKDCDCLHVVEPMPVRGPDVEAYCLRCECKYEERSSVTIKVT
IIIIYLSILGLLLLYMVYLTLEPILKRRLFGHAQLIQSDDDIGDHQPF
ANAHDVLA SRSRANVLNKVEYAQQRWKLQVQEQ RKS
VFD RHVVLS

FIGURE 301

GCACCTGCGACCACCGTGAGCAGTC**ATG**GCGTACTCCACAGTGCAGAGAGTCGCTCTGGCTT
 CTGGGCTTGTCTGGCTCTGTGCTGCTGCTGCCAAGGCCTTCCTGTCCCGCGGAAGCGG
 CAGGAGCCGCCGCCGACACCTGAAGGAAAATTGGGCCGATTTCACCTATGATGCATCATCA
 CCAGGCACCCTCAGATGGCCAGACTCCTGGGGCTCGTTTCCAGAGGTCTCACCTTGCCGAGG
 CATTTGCAAAGGCCAAAGGATCAGGTGGAGGTGCTGGAGGAGGAGGTAGTGGGAAGAGGTCTG
 ATGGGGCAGATTATTCCAATCTACGGTTTTGGGATTTTTTATATATACTGTACATTCTATT
 TAAGGTAAGTAGAATCATCCTAATCATATTACATCA**TGA**AAATCTAATATGGCGATAAAAA
 TCATTGTCTACATTA AAACTTCTTATAGTTCATAAAATTATTTCAAATCCATCATCTCTTTA
 AATCCTGCCTCCTCTTCATGAGGTACTTAGGATAGCCATTATTTCAAGTTTCACATAAGAATG
 TTTACTCAATGTTTAAAGTGTTTTGCCCAAAATTCACAACTACAAGGCAGAACTAGGACTT
 GAACATGGATCTTTTGGTTCCTAATCCAGTGAGTGATACAATTCAATGCACTCCCTGCCA

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MAYSTVQRVALASGLVLALSLLLPKAFLSRGKRQEPPTPEGKLGFRFPPMMHHHQAPSDGQT
 PGARFQRSHLAEAFKAKGSGGGAGGGSGRGLMGQIIPIYGFIFLYILYILFKVSRRIILI
 ILHQ

FIGURE 303

CGGCTCGAGTGCAGCTGTGGGAGATTTTCAGTGCATTGCCTCCCCGCGGTGCTCTTCATCTT
GGATTGAAAGTTGAGAGCAGC**ATG**TTTTTGCCCACTGAAACTCATCTGCTGCCAGTGTTAC
TGGATTATTCCTTGGGCTGAATGACTTGAATGTTTCCCGCCTGAGCTAACAGTCCATGTG
GGTGATTTCAGCTCTGATGGGATGTGTTTTCCAGAGCACAGAAGACAAATGTATATTCAAGAT
AGACTGGACTCTGTACCAGGAGAGCACGCCAAGGACGAATATGTGCTATACTATTACTCCA
ATCTCAGTGTGCCTATTGGGCGCTTCCAGAACCAGCTACACTTGTATGGGGACATCTTATGC
AATGATGGCTCTCTCTGCTCCAAGATGTGCAAGAGGCTGACCAGGGAACCTATATCTGTGA
AATCCGCCTCAAAGGGGAGAGCCAGGTGTTCAAGAAGGCGGTGGTACTGCATGTGCTTCCAG
AGGAGCCCAAAGAGCTCATGGTCCATGTGGGTGGATTGATTGAGTGGGATGTGTTTTCCAG
AGCACAGAAGTGAACACGTGACCAAGGTAGAATGGATATTTTCAGGACGGCGCAAAGGA
GGAGATTGTATTTTCGTTACTACCACAACTCAGGATGTCTGTGGAGTACTCCAGAGCTGGG
GCCACTTCCAGAATCGTGTGAACCTGGTGGGGACATTTTCCGCAATGACGGTCCATCATG
CTTCAAGGAGTGAGGGAGTCAGATGGAGGAACTACACCTGCAGTATCCACCTAGGGAACCT
GGTGTTCAGAAAACCATTTGTGCTGCATGTGACCCCGAAGAGCCTCGAACACTGGTGACCC
CGGCAGCCCTGAGGCCCTCTGGTCTTGGGTGGTAATCAGTTGGTGATCATTTGTGGGAATTGTC
TGTGCCACAATCTGCTGCTCCCTGTTCTGATATTGATCGTGAAGAAGACCTGTGGAAATAA
GAGTTCAGTGAATCTACAGTCTTGGTGAAGAACACGAAGAAGACTAATCCAGAGATAAAG
AAAAACCTGCCATTTTGAAGATGTGAAGGGGAGAAACACATTACTCCCAATAATTGTA
CGGGAGGTGATCGAGGAAGAAGAACCAAGTGAAAAATCAGAGGCCACCTACATGACCATGCA
CCCAGTTTGGCCTTCTCTGAGGTCAGATCGGAACAACCTCACTTAAAAAAGTCAGGTGGGG
GAATGCCAAAAACACAGCAAGCCCTTT**TGA**GAGAATGGAGAGTCCCTTCATCTCAGCAGCGG
TGGAGACTCTCTCTGTGTGTCTCTGGGCCACTCTACCAGTGATTTTCAGACTCCCGCTCTC
CCAGCTGTCTCTGTCTCATTGTTTGGTCAATACACTGAAGATGGAGAATTTGGAGCCTGG
CAGAGAGACTGGACAGCTCTGGAGGAACAGGCCCTGCTGAGGGGAGGGGAGCATGGACTTGGC
CTCTGGAGTGGGACACTGGCCCTGGGAACCAGGCTGAGCTGAGTGGCCTCAAACCCCCGTT
GGATCAGACCTCTGTGGGAGGTTCTTAGTGGATGAGTTACTGGGAAGAATCAGAGATA
AAAACCAACCCAAATCAA

FIGURE 304

MFCPLKLILLPVLLDYSLGLNDLNVSPPELTVHVGDSALMGCVFQSTEDKCIFKIDWTLSPG
EHAKDEYVLYYYYNLSVPIGRFQNRVHLMGDILCNDGSLLLQDVQEADQGTYICEIRLKGES
QVFKKAVVLHVLPEEPKELMVHVGGLIQMGCVFQSTEVKHVTKVEWIFSGRRAKEEIVFRYY
HKLRMSVEYSQSWGHFQNRVNLVGDIFRNDGSIMLQGVRESGGNYTCSIHLGNLVFKKTIV
LHVSPEEPRTLVTPAALRPLVLGGNQLVIIVGIVCATILLPLVLILIVKKTGKSSVNSTV
LVKNTKKTNPETKEKPKCHFERCEGEKHIYSPIIVREVIEEEEPSEKSEATYMTMHPVWPSLR
SDRNNLEKKSGGGMPKTQQAF

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FIGURE 305

CTATGAAGAAGCTTCCTGGAAAACAATAAGCAAAGGAAAACAAATGTGTCCCATCTCACATG
 GTTCTACCCCTACTAAAGACAGGAAGATCATAAACTGACAGATACTGAAATTGTAAGAGTTGG
 AAACACATTTTGCAAAGTCATTGAACTCTGAGCTCAGTTGCAGTACTCGGGAAGCCATGCA
 GGATGAAGATGGATACATCACCTTAAATATTTAACTCGGAAACCAGCTCTCGTCTCCGTTG
 GCCCTGCATCCTCCTCCTGGTGGCGTGTGATGGCTTTGATTCTGCTGATCCTGTGCGTGGGG
 ATGGTTGTCGGGCTGGTGGCTCTGGGGATTTGGTCTGTGCATGCAGCGCAATTACCTACAAGA
 TGAGAATGAAAATCGCACAGGAAGCTCTGCAACAATTAGCAAAGCGCTTCTGTCAATATGTGG
 TAAACAATCAGAACTAAAGGGCACTTTCAAAGGTCATAATGCAGCCCCCTGTGACACAAAC
 TGGAGATATTATGGAGATAGCTGCTATGGGTTCTTCAGGCACAACCTTAACATGGGAAGAGAG
 TAAGCAGTACTGCACTGACATGAATGCTACTCTCCTGAAGATTGACAACCGGAACATTGTGG
 AGTACATCAAAGCCAGGACTCATTTAATTCGTTGGGTCGGATTATCTCGCCAGAAGTCGAAT
 GAGGTCTGGAAGTGGGAGGATGGCTCGGTTATCTCAGAAAATATGTTTGAGTTTTTGAAGA
 TGGAAAAGGAAATATGAATTGTGCTTATTTTCATAATGGGAAAATGCACCCTACCTTCTGTG
 AGAACAACATATTATTTAATGTGTGAGAGGAAGGCTGGCATGACCAAGGTGGACCAACTACCT
TAATGCAAAGAGGTGGACAGGATAACACAGATAAGGGCTTTATTGTACAATAAAAGATATGT
 ATGAATGCATCAGTAGCTGAAAAAAAAAAAAA

FIGURE 306

MQDEDGYITLNIKTRKPALVSVGPASSSWVRVMAILLILCVGMVVGLVALGIWSVMQRNYL
QDENENRTGTLQQLAKRFCQYVVKQSELKGTFKGHKCSPCDTNWRYYGDSYGFRRHNLWE
ESKQYCTDMNATLLKIDNRNIVEYIKARTHILRWVGLSRQKSNEVWKWEDGSVISENMFEFL
EDGKGNMNCAYFHNGKMHPTFCENKHYLMCERKAGMTKVDQLP

FIGURE 307

CCCACGCGTCCGCGCAGTTCGCGCAGTTCTGCCTCCGCTGCCAGTCTCGCCCGCATCCCGG
 CCGGGGCTGTGGCGTCGACTCCGACCCAGGCAGCCAGCAGCCCGCGCGGGAGCCGGACCGC
 CGCCGGAGGAGTTCGGACGGCATGCTGAGCCCCCTCCTTTGCTGAAGCCCGAGTGC GGAGAA
 GCCCCGGGCAAAACGACGCTAAGGAGACAAAGCGGCGAAGTTCGCGAGACAGCGGACAAGCAG
 CGGAGGAGAAGGAGGAGGAGGCGAACCAGAGAGGGGCAGCAAAAGAAGCGGTGGTGGTGGG
 CGTCGTGGCC**ATG**GCGGCGGCTATCGCCAGCTCGCTCATCCGTGAGAAGAGGCAAGCCCGCG
 AGCGCGAGAAATCCAACGCCTGCAAGTGTGTGAGCAGCCCCAGCAAGGCAAGACCAGCTGC
 GACAAAAACAAGTTAAATGTCTTTTCCCGGTCAAACCTCTTCGGCTCCAAGAAGAGGCGCAG
 AAGAAGACCAGAGCCTCAGCTTAAGGGTATAGTTACCAAGCTATACAGCCGACAAGGCTACC
 ACTTGCAGCTGCAGGCGGATGGAACCATTGATGGCACCAAGATGAGGACAGCACTTACACT
 CTGTTTAACCTCATCCCTGTGGGTCTGCGAGTGGTGGCTATCCAAGGAGTTCAAACCAAGCT
 GTACTTGGCAATGAACAGTGAAGGATACTTGTTACACCTCGGAACCTTTTACACCTGAGTGCA
 AATTCAAAGAATCAGTGTGTTGAAAATTATTATGTGACATATTCATCAATGATATACCGTCAG
 CAGCAGTCAGGCCGAGGGTGGTATCTGGGTCTGAACAAAGAAGGAGAGATCATGAAAGGCAA
 CCATGTGAAGAAGAACAAGCCTGCAGCTCATTTTCTGCCTAAACCACTGAAAGTGGCCATGT
 ACAAGGAGCCATCACTGCACGATCTCACGGAGTCTCCCGATCTGGAAGCGGGACCCCAACC
 AAGAGCAGAAGTGTCTCTGGCGTGCTGAACGGAGGCAAAATCCATGAGCCACAATGAATCAAC
GTAGCCAGTGAGGGCAAAAGAAGGGCTCTGTAACAGAACCTTACCTCCAGGTGCTGTTGAAT
 TCTTCTAGCAGTCCTTCACCCAAAAGTTCAAATTTGTGAGTACATTTACCAACAAACAGG
 CAGAGTCACTATTCTATCTGCCATTAGACCTTCTTATCATCCATACTAAAGC

FIGURE 308

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA28498
><subunit 1 of 1, 245 aa, 1 stop
><MW: 27564, pI: 10.18, NX(S/T): 1
MAAAIASSLIRQKRQAREREKSNACKCVSSPSKGTSCDKNKLNVF SRVKLFGSKKRRRRRP
EPQLKGIVTKLYSRQGYHLQLQADGTIDGTDKDEDSTYTLFNLI PVGLRVVAIQGVQTKLYLA
MNSEG YLYTSELTPECKFKESVFENYYVTYSSMIYRQQSGRGWYLG LNKEGEIMKGNHVK
KNKPAAHFLPKPLKVAMYKEPSLHDLTEFSRSGSGTPTKSRSVSGV LGGKSM SHNEST
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N-glycosylation site.

amino acids 242-246

Glycosaminoglycan attachment site.

amino acids 165-169, 218-222

Tyrosine kinase phosphorylation site.

amino acids 93-100

N-myristoylation site.

amino acids 87-93, 231-237

ATP/GTP-binding site motif A (P-loop).

amino acids 231-239

HBGF/FGF family proteins

amino acids 78-94, 102-153

FIGURE 309

CCAGGATGGAGCTGGGGCCTGTATAGCCATATTATTGTTCTATGCTACTAGACATGGGGGGG
 ACTTGGTGAAAAAGGTATTATCCAGCCAGAGGGTCTGGGAGCCCTGTCTTACTGAACCTGGG
 CAACCTGGATATTCTGAGACATATTTTGGGGGATTTTCAGTGAAAAAGTGGGGGATCCCCCT
 CCATTTAGAGTGTAGCAAAGGAAAAAACCAAGGTTGGGTTCCCTTCTGACATTGGCAGTG
 CCCCAGTAGGGGTGGGATGAGCGAATATTTCCCAAAGCTAAAGTCCACACCTGTAGATTAC
 AAGAGTGGATTTTGGCAGGAGTGTGCCCCAAAATACAGTGGAAAGTGCCTGAAGATATTTAA
 ACCACGCTCTTGGAAATTTAGTGGGTCTTGGCTTTGGGATAGGTGAAGTGAGGACAGACACTG
 GAGAGGAGGGAAGGGGACGTTTTCAATAGGAGGCAAACTCGAGGGTGGGATCCACTGAGG
 AGTACATAGGCTGCTGGATCTGGTGGAGCCAGCACTGGGCCCACGGGTGGTAACCTGGCTGCT
 GTGGAGGGGGGTACGTGAGGGGGGGGTCTGGGGCTTATCCTCAGGTCTGTGGGTGGGGCAG
 CGAGTCGGGGCCTGAGCGTCAAGAGCATGCCCTAGTGAGCGGGCTCCTCTGGGGGAGCCAG
 CGCGCTCCGGGCGCCTGCCGGTTTGGGGGTGTCTCCTCCCGGGGCGCT**ATGG**GCGGCGTGGC
 CAGTAGCCTGATCCGCGAGAAGCGGGAGGTCCGCGAGCCCGGGGGCAGCCGGCCGGTGTCCG
 CGCAGCGGCGCGTGTGTCCCCGCGGCACCAAGTCCCTTTGCCAGAAGCAGTCCCTCATCCTG
 CTGTCCAAGGTGCGACTGTGCGGGGGGCGGCCGCGCGGCCGACCGCGGCCCGGAGCCTCA
 GCTCAAAGGCATCGTCACCAAAGTGTCTGCCGCCAGGGTTTCTACCTCCAGGCGAATCCCG
 ACGGAAGCATCCAGGGCACCCAGAGGATACCAGTCCCTTCAACCACTTCAACCTGATCCCT
 GTGGGCCCTCCGTGTGGTCAACATCCAGAGCGCCAAGCTGGGTACTACATGGCCATGAATGC
 TGAGGGACTGCTCTACAGTTCGCCGCATTTACAGCTGAGTGTGCGCTTTAAGGAGTGTGTCT
 TTGAGAATTACTACGTCTGTACGCCTCTGCTCTTACC GCCAGCGTCTTCTGGCCGGGCC
 TGGTACCTCGGCCTGGACAAGGAGGGCCAGGTATGAAGGAAACCGAGTTAAGAAGACCAA
 GGCAGCTGCCACTTTCTGCCAAGCTCCTGGAGGTGGCCATGTACCAGGAGCCTTCTCTCC
 ACAGTGTCCCGAGGCCTCCCTTCCAGTCCCCCTGCCCC**TGA**AATGTAGTCCCTGGACTG
 GAGGTTCCCTGCACTCCAGTGAGCCAGCCACCACCACAACCTGT

FIGURE 310

MAALASSLIRQKREVREPGGSRPVSAQRRVCPRGTSKLCQKQLLILLSKVRLCGGRPARPDR
GPEPQLKGIVTKLFCRQGFYLANPDGSIQGTPEDTSSFTHFNLIPVGLRVVTIQSAKLGHY
MAMNAEGLLYSSPHFTAECRFKECVFENYYVLYASALYRQRSGRAWYLGLDKEGQVMKGNR
VKKTKAAAHFLPKLLEVAMYQEPSLHSVPEASPSSEPPAP

Tyrosine kinase phosphorylation site:

amino acids 199-207

N-myristoylation sites:

amino acids 54-60, 89-95, 131-137

HBGF/FGF family signature:

amino acids 131-155

FIGURE 311

ATGGCCGCGGCCATCGCTAGCGGCTTGATCCGCCAGAAGCGGCAGGCGGGAGCAGCACTG
GGACCGGCCGTCTGCCAGCAGGAGGCGGAGCAGCCCCAGCAAGAACCGCGGGCTCTGCAACG
GCAACCTGGTGGATATCTTCTCCAAAGTGCGCATCTTCGGCCTCAAGAAGCGCAGGTTGCGG
CGCCAAGATCCCAGCTCAAGGGTATAGTGACCAGGTTATATTGCAGGCAAGGCTACTACTT
GCAAATGCACCCGATGGAGCTCTCGATGGAACCAAGGATGACAGCACTAATTCTACACTCT
TCAACCTCATACCAGTGGGACTACGTGTTGTTGCCATCCAGGGAGTAAAAACAGGTTGTAT
ATAGCCATGAATGGAGAAGGTTACCTCTACCCATCAGAACTTTTTACCCCTGAATGCAAGTT
TAAAGAATCTGTTTTTGAAAATTATTATGTAATCTACTCATCCATGTTGTACAGACAACAGG
AATCTGGTAGAGCCTGGTTTTTGGGATTAAATAAGGAAGGCAAGCTATGAAAGGGAACAGA
GTAAAGAAAACCAACCAGCAGCTCATTTTCTACCCAAGCCATTGGAAGTTGCCATGTACCG
AGAACCATCTTTGCATGATGTTGGGGAACGGTCCCAGAGCCTGGGGTGACGCCAAGTAAAA
GCACAAGTGCGTCTGCAATAATGAATGGAGGCAAACCAAGTCAACAAGAGTAAGACAACA**TAG**

FIGURE 312

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA28503

><subunit 1 of 1, 247 aa, 1 stop

><MW: 27702, pI: 10.36, NX(S/T): 2

MAAAIASGLIRQKRQAREQHWDREPSASRRRSSPSKNRGLCNGNLVDIFS KVRIFGLKKRRLR
 RQDPQLKGIVTRLYCRQGYLQMHPDGALDGT KDDSTNSTLFNLIPVGLRVVAIQGVKTGLY
 IAMNGEGYLPSELTPECKFKESVFENYYVIYSSMLYRQQESGRAWFLGLNKEGQAMKGNR
 VKKTKPAAHFLPKPLEVAMYREPSLHDVGETVPKPGVTPSKSTSASAIMNGGKPVNKS KTT

N-glycosylation site.

amino acids 100-104, 242-246

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 28-32, 29-33

Tyrosine kinase phosphorylation site.

amino acids 199-207

N-myristoylation site.

amino acids 38-44, 89-95, 118-124, 122-128, 222-228

HBGF/FGF family proteins.

amino acids 104-155, 171-198

FIGURE 313

GGGGAGAGSAATTGACCATGTAAAAGGAGACTTTTTTTTTTGGTGGTGGTGGCTGTGGGTGCCTTGCAAAAAAT
 GAAGGATGCAGGACGACGCTTTCTCCTGGAACCGAACGCAATGGATAAAGTATTGTGCAAGAGAGAAGGAAGA
 ACGAAGCTTTTTCTGTGAGCCCTGGATCTTAACACAAATGTGTATATGTGCACACAGGGAGCATTCAAGAATG
 AATAAACCAGAGTTAGACCCCGGGGGTGTGGTGTCTGCATATAAATAATATCTTAAGCAGCTGTTCCC
 CTCCTCCACCCCAAAAAAAGGATGATTGGAATGAAGAACCAGGATTACAAAGAAAAAGTATGTTCAATT
 TTCTCTATAAAGGAGAAAGTGAGCCAGGAGATATTTTTGGAATGAAAGTTTGGGGCTTTTTAGTAAAGTAA
 AGAATCTGGTGTGGTGTGTTTTCTTTCTTTTTGAATTTCCACAAAGAGGAGAGAAATTAATAATACATCTGC
 AAAGAAATTTAGAGAAGAAAAGTTGACCGCGGAGATTGAGGCATTGATTGGGGGAGAGAAACCGCAGAGCA
 CAGTTGGATTTGTGCCTATGTTGACTAAAATGACGGATAATTGACGTTGGATTTTTCTTCATCAACCTCCTTT
 TTTTTAAATTTTTATTCTTTTGGTATCAAGATCATGCGTTTTCTCTTGTCTTAACCCAGCTGGATTCCATCT
 GGATGTTGCTGTGATCAGTCTGAATACAACTGTTGAATCCAGAAGGACCAACACAGATAAATATGAATG
 TTGAACAAGATGACCTTACATCCACAGCAGATAATGATAGGCTTAGGTTTAACAGGGCCCTATTGACCCCT
 GCTTGTGGTGTGCTGTGCTGCTTCAACTTCTTGTGGTGGCTGGTCTGGTGGGGCTCAGACCTGCCCTTGTGT
 GCTCCTGCAGCAACGATTGAGCAAGGTGATTTGTGTTTCGAAAAACCTGCGTGAGGTTCCGGATGGCATCTCC
 ACCAACACACCGGCTGTGAACCTCCATGAGAACCAGATCATCAAGTGAACAGCTTCAAGCACTTGAG
 GCACCTTGAATACTCAGATTGAGTAGGAACCATATCAGAACCATGAAATGGGGCTTTCAATGGTCTGGCGA
 ACCTCAACACTCTGGAACCTTTGACATCGTCTTACTACCATCCGAATGGAGCTTTGTATACCTGTGCTAAA
 CTGAAGGAGCTCGTTGCGAAACACCCCATGAAAGCATCCCTTCTTATGCTTTTAACAGAATTCTCTCTTT
 GCGCGACTAGACTTAGGGGAATTGAAAGACTTTATACATCTCAGAAGGTGCTTTGAAGTCTGCTCAACT
 TGAGGTATTTGAACCTTGCCATGTCAACCTTCGGGAAATCCCTAACCTCACACCGCTCATAAACTAGATGAG
 CTGGATCTTTCTGGGAATCATTTATCTGCCATCAGGCTGGCTTTCCAGGGTTTGATGCACCTTCAAAAAT
 GTGGATGATACAGTCCAGATTCAAGTGATTGAACGGAATGCCTTGAACACCTTCAGTCACTAGTGAGATCA
 ACCTGGCACACAATAATCAACATTACTGCCTCATGACCTCTTCACTCCCTGTCATCATCTAGACGGATACAT
 TTACATCACAAACCTTGAACCTGTAACTGTGACATACTGTGGCTCAGCTGTTGAGATAAAAGCATGGCCCCCTC
 GAACACAGCTTGTGTGCGCGGTGTAACACTCCTCCCAATCTAAAGGGGAGGTACATTGGAGAGCTCGACAGCA
 ATTACTTACATGCTATGCTCGGCTGATTGTGGAGCCCCCTGCAGACCTCAATGTCACTGAAGGCATGGCAGCT
 GAGCTGAAATGTCGGGCTCCACATCCCTGACATCTGTATCTTGGATTACTCCAATGGAACAGTCAATGACACA
 TGGGGCTACAAAGTGGGATGCTGTGCTCAGTATGTTAGCTTAAATTTACAAATGTAACCTGTGCAAGATA
 CAGGCTGTACACATGTATGTTGAGTAATTCGGTTGGGAATACTACTGCTTCAGCCACCTGAATGTTACTGCA
 GCAACCACTACTCCTTTCTTACTTTTCAACCGTCACAGTAGAGACTATGGAACCGCTCAGGATGAGGACAG
 GACCACAGATACAATGTGGGTCCCACTCCAGTGGTCGACTGGGAGACCAATGTGACCACCTCTCTCACAC
 CACAGAGCACAAGGTGCAGAGAGAAACCTTCAACATCCAGTGACTGATATAACAGTGGGATCCAGGAATT
 GATGAGGTCATGAAGACTACCAAAATCATCATTTGGGTGTTTTGTGGCCATCACACTCATGGCTGCAGTGATGCT
 GGTCAATTTCTACAAGTAGGGAAGCAGCACCATCGGCAAAACCATCACGCCCCAACAGGACTGTTGAAATTA
 TTAATGTGGATGATGAGATTACGGGAGACACACCATGGAAGGCCACTGCCCATGCTGCTATCGAGCATGAG
 CACCTAAATCACTATAACTCATACAAATCTCCCTTCAACCACACAACAAGTAAACAAATAAATCAATACA
 CAGTTTCAGTGCATGAACCTTATTGATCCGAATGAACCTTAAGAGACAATGTACAGAGACTCAAACTCTAAACAA
 TTTACAGAGTTACAAAAAACAAACAAATCAAAAAAAGACAGTTTATTAATAATGACACAATGACTGGGCTAA
 ATCTACTGTTTCAAAAAGTGTCTTTACAAAAAACAAAAAGAAAGAAATTTATTTATTAATAATCTATTG
 TGACTTAAGCAGACAAAAA

FIGURE 314

MLNKMTLHPQQIMIGPRFNALFDPLLVLALLQQLLVVAGLVRAQTCPSCVSCSNQFSKVIC
 VRKNLREVPDGISTNTRLNLHENQIQIKVNSFKHLRHLEILQLSRNHIRTIEIGAFNGLA
 NLNLTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
 YISEGAFEGLSNLRVYNLAMCNLREIPNLTPLIKLELDELDSGNHLSAIRPGSFQGLMHLQKL
 WMIQSQIQVIERNAFDNLQSLVEINLAHNNLTLLPHDLFTPLHHLERIHLLHNPWNCNCDIL
 WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNVTEGMAAE
 LKCRASLTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTNLNFTNVTQDTGMYTCMVNSVGN
 TTASATLNVTAAATTPFSYFSTVTMETPSQDEARTDNNVGPTPVVDWETTNVTTSLTPQ
 STRSTKFTTIPVTDINSIGIPGIDEVMKTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRRQN
 HHAPTRTVEIINVDEITGDTPMESHLMPAIEHEHLNHNYSYKSPFNHTTVNTINSIHSS
 VHEPLLIRMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419,
 434-438, 442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
 391-397, 422-428, 433-439, 531-537

FIGURE 315

CGCGCGGGGAGCCCATCTGCCCCAGGGGCACAGGGCGCGGGGCCGGTCTCCGCCCGGCACAT
GGCTTGCAGCCACCTCGCGGACACCCAGGAGCGCCGCGCCAGCTCGCCCGAGGCTCCGTCCGA
GGCGCCGGCGCGCCCGGAGCCCAAGCAGCAACTGACGGGGAAGCGCCGCGCTCCGGGATC
GGC**ATG**TCCCTCCTCTCTCTCTTGTCTAGTTTCTCTACTATCTTGGAACCTTGGGGACTCA
CACTGAGATCAAGAGATGGCAGAGAAAGGTCTACTTGGCCCTGCCACCATCACTGGGG
TTCAGAAAAAGACACTCTGGATATGTAATGGCTGCTCACCAGATATGAAGGGAACCAAAAA
GTGGTGATCACTTACTCCAGTCTGATCTGTACATAACTTGACTGAGGAACAGAAAGGCCG
AGTGGCCTTTTGCTTCAAATTTCTGCGAGGAGATGCCTCTTCAGATGAACCTCTGAAG
CCAGTGTAGAGGGCGGTATACCTGTAAAGTTAAGAATTACGGGCGCTACGTGTGGAGCCAT
GTCTATCTTAAAGCTCTTAGTGAGACATCCAAAGCCAAAGTGTGAGTTGGAAGGAGAGCTGAC
AGAAGGAAGTGAAGCTGAGTTTGCAGTGTGAGTCTCCTTGCCAGAGGCCATTGTGTATTT
ACTGGCAGCGAATCCGAGAGAAAGAGGGAGAGATGAACGTCTGCCTCCAAATCTTAGGATT
GACTACAAACACCTCGACGAGTTCTGTGAGAATCTTACCATTCTCTGACTGTA
CCAGTGCACAGCGAGGCAAGAGCTGGGAAGGAAGCTGTGGTGGCGAGTAACGTACAGT
ATGTACAAGCATCCGATCGGATGGTTGCGAGGACAGTGAAGCAGTATGGCTGGAGCCCTGCTG
ATTTTCTCTTGGTGTGCTGCTAATCCAAAGGAAGACAAAGAAAGATATGAGGAAGAAGA
GAGACCTAATGAAATTCGAGAAGATGCTGAAGCTCCAAAGCCCGTCTTGTGAACCCAGCT
CCTCTTCTCTGAGCTCTCGGAGCTACGCTCTGGTTTCTTCTCTCCATCGCTCCACAGAAAT
AGTGCTCACGCGACGCGGACACTGTCAACTGACGCAAGCCACCGAGGGCTGGCCAC
CCAGGCGATACAGCTAGTGGGCGAGAGTGAAGGTTCTGAACCAAGAAAGTCCACCATG
CTAATCTGACCAAGCAGAAACACAGGCTCCAGCATGATCCCCAGCCAGAGCAGCTTCCAA
ACGGTCT**TGA**ATTACAATGGACTGATCCACGCTTTCCTAGGATCAGGGTCTTTTGGACTC
TTCTCGTCACTTGAGCTCAAGTCAAGCCACAGCACACACAGCATGAGAGTCTATTAAGTACAA
GTGACGATTGCGCGGAACAGATTCAATGAGCATTTTCTTATACATCAACAAAGCAAA
AGGATGTAAGCTGATTCTGTAAAAAGGCATCTTATTGTGCCTTTAGACCAGATGAAGG
AAAGCGAGGATCCAAATCTATTTTGTGACAGGACCTGGTGTGAAGAGGTTGGGGAAAGGTG
AGGTAATATACCTAAAACTTTTAATGGGGATATTTGTATCAGTGGCTTTGATTACAAAT
TTCAAGAGGAATGGGATGCTGTTTGAATTTTCTGATCATTTCTGCAAACTATTGGATT
ATTAGTTATTCAAGAGCTCAAGCAGAACCCAGCCTTATTACACCTCTACACAGTGAT
TGAGCTAACCACTTCTAAGAAACTCCAAAAAGGAACATGTGTCTTCTATTCTGACTTAAC
TCTATTGTCTATAAGGTTTGGATATTAATTAATCGAGGGATGTGAATAGTGGGAGATGGAGA
AGAGTGAATGAGTTTCTCCACTCTATCTAATCTCACTATTGTATTGAGCCCAAAATAC
TATGAAGGAGACAAAAATTTGTGAACAAGGATTTGGAAGAGCTTTCATCTCTATGATGTT
ATGAGGATTTGTTGACAAACATAGAAATATATAATGGAGCAATTTGGATTTCCTCCATAAT
CAGATGCCCTCAAGGACTTCTGCTAGATATTTCTGGAAGGAGAAATACAACTGTCATT
TATCAACGTCTTTAGAAGAAATTTCTCTAGAAAAAAGGATCTAGGAATGCTGAAAGATT
CCCAACATTCATTATAGTCTCTCTTTCTTGAAAAATGTGAACCAAGAAATGCAAGACTGG
GTGGACTAGAAAGGGAGATTAGATCAGTTTTCTCTTAATATGTCAAGGAAGGTAGCCGGCA
TGGTGCCAGGCACCTTGAGAAAATCCAGAGTTGGAGGTGCAGTGAGCCGAGATTATGCC
ATTGACTCTCAGCTGGGTGACAGAGCGGACTCCGCTC

FIGURE 316

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45419

><subunit 1 of 1, 373 aa, 1 stop

><MW: 41281, pI: 8.33, NX(S/T): 3

MSLLLLLLLLVSYYVGTGLGTHTEIKRVAEEKVTLPCHHQLGLPEKDTLDIEWLLTDNEGNQKV
VITYSSRHVYNNLTTEEQKGRVAFASNFLAGDASLQIEPLKPSDEGRYTCKVKNSGRYVWSHV
ILKVLVRPSKPKCELEGELTEGSDTLQCESSSGTEPIVYYWQRIREKEGEDERLPPKSRID
YNHPGRVLLQNLTMSYSGLYQCTAGNEAGKESCVVRVTVQYVQSIGMVAGAVTGIVAGALLI
FLLVWLLIRRKDKERYEEEEERPNEIREDAEAPKARLVKPSSSSSGSRSSRSRSGSSSTRSTANS
ASRSQRTLSTDAAPQPGLATQAYSLVGPEVRGSEPKKVHHANLTKAETTPSMIPSQSRAFQTV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 232-251

[illegible]

FIGURE 318

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA82361
><subunit 1 of 1, 352 aa, 1 stop
><MW: 38938, pI: 7.86, NX(S/T): 3
MALLLCFVLLCGVDFARSLSTITPEEMIEKAKGETAYLPCKFTLSPEDQGGLDIEWLISPA
DNQKVDQVILIYSGDKIYDDYYPDLKGRVHFTSNDLKSGDASINVTNLQLSDIGTYQCKVKK
APGVANKKIHLVVLVKPSGARCYPDVGSEEIGSDFKIKCEPKEGSLPLQYEWQKLSDSQKMPT
SWLAEMTSSVISVKNASSEYSGTYSCTVRNRVGSQCLLRNLNVPPSNKAGLIAGAIIGTLL
ALALIGLII FCCRKKRREEKYKEVHHDIREDVPPPKSRTSTARSYIGSNHSSLGSMSPSNM
EGYSKTQYNQVPSEDFERTPQSPTLPPAKFKYPYKTDGITVV

Signal sequence.

amino acids 1-19

Transmembrane domain:

amino acids 236-257

N-glycosylation sites.

amino acids 106-110, 201-205, 298-302

Tyrosine kinase phosphorylation sites.

amino acids 31-39, 78-85, 262-270

N-myristoylation sites.

amino acids 116-122, 208-214, 219-225, 237-243, 241-247,
245-251, 296-302

Myelin P0 protein.

amino acids 96-125

FIGURE 319

TGAATGACTTCCACGGCTGGGACGGGAACCTTCCACCCACAGCTATGCCTCTGATTTGGTGA
 ATGGTGAAGTGCCTGTCTAACTTTTCTGTAAAAAGAACAGCTGCCTCCAGGCAGCCAGCC
 CTC AAGCATCACTTACAGGACCAGAGGGACAAGACATGACTGTGATGAGGAGCTGCTTTTCGC
 CAATTTAACACCAAGAAGAATTGAGGCTGCTTGGGAGGAAGGCCAGGAGGAACACGAGACTG
 AGAGATGAATTTTCAACAGAGGCTGCAAGCCTGTGGACTTTAGCCAGACCCTTCTGCCCTC
 CTTTCTGCTGGCGACAGCCTCTCAAATGCAGATGGTTGTGCTCCCTTGCCTGGGTTTTACCCTG
 CTTCTCTGGAGCCAGGTATCAGGGGCCAGGGCCAAGAATTCCACTTTGGGCCCTGCCAAGT
 GAAGGGGGTTGTTCCCGAAGAACTGTGGGAAGCCTTCTGGGCTGTGAAAGACACTATGCAAG
 CTCAGGATAACATCACGAGTGCCCGGCTGCTGCAGCAGGAGGTTCTGCAGAACGCTCTCGGAT
 GCTGAGAGCTGTTACCTTGTCCACACCCTGCTGGAGTTCTACTTGAAACTGTTTTCAAAAA
 CCACCACAATAGAACAGTTGAAGTCAGGACTCTGAAGTCATTCTCTACTCTGGCCACAACCT
 TTGTTCTCATCGTGTCAACCTGCAACCAGTCAAGAAAATGAGATGTTTTCCATCAGAGAC
 AGTGCACACAGGCGGTTTCTGCTATTCCGGAGAGCATTCAAACAGTTGGACGTAGAAGCAGC
 TCTGACCAAGGCCCTTGGGGAAGTGGACATTCTTCTGACCTGGATGCAGAAATTTCTACAAGC
 TCTGAATGTCTAGACCAGGACCTCCCTCCCCCTGGCACTGGTTTGTTCCTGTGTCAATTCA
 AACAGTCTCCCTTCCATATGCTGTTCACTGGGACACTTCACGCCCTTGGCCATGGGTCCCATT
 TTGGCCCAGGATTATTGTCAAAGAAGTCATTCTTTAAGCAGCGCCAGTGACAGTCAGGGAAG
 GTGCCCTCTGGATGCTGTGAAGAGTCTACAGAGAAGATTCTTGATTTATTACAACCTCTATTT
 AATTAATGTCAGTATTTCAACTGAAGTTCTATTTATTTGTGAGACTGAAGTTACATGAAGG
 CAGCAGAATATTGTGCCCATGCTTCTTTACCCCTCACAATCCTTGCCACAGTGTGGGGCAG
 TGGATGGGTGCTTAGTAAGTACTTAATAAACTGTGGTGCTTTTTTTGGCCTGTCTTTGGATT
 GTTAAAAAACAGAGAGGGATGCTTGGATGTAAAACTGAACCTCAGAGCATGAAATCACACT
 GTCTTCTGATATCTGCAGGGACAGAGCATTGGGGTGGGGTAAGGTGCATCTGTTTGAAGG
 TAAACGATAAAATGTGGATTAAAGTGCCAGCACAAAGCAGATCCTCAATAAACATTTTCATT
 TCCCACCCACACTCGCCAGCTCACCCATCATCCCTTCCCTTGGTGCCTCCTTTTTTTTTT
 TATCCTAGTCATTCTTCCCTAATCTTCCACTTGAGTGTCAGCTGACCTTGTGATGGTGAC
 ATTGCACCTGGATGTACTATCCAATCTGTGATGACATTCCCTGCTAATAAAAGACAACATAA
 CTCCAAAAA

FIGURE 320

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA88002

><subunit 1 of 1, 206 aa, 1 stop

><MW: 23799, pI: 9.12, NX(S/T): 3

MNFQQRLQSLWTLARPFPCPLLATASQMQMVVLPCLGFTLLLSQVSGAQGQEFHFGPCQVK
GVVPQKLWEAFWAVKDTMQAQDNITSARLLQQEVLQNVSDAESCYLEVHTLLEFYLKTVFKNH
HNRTVEVRTLKSFSTLANNFVLIVSQLQPSQENEMFSIRDSAHRRFLLFRRAFKQLDVEAAL
TKALGEVDILLTWMQKFYKL

Signal sequence:

amino acids 1-42

N-glycosylation sites.

amino acids 85-89, 99-103, 126-130

FIGURE 321

AAGGAGCAGCCCGCAAGCACCAAGTGAGAGGCATGAAGTTACAGTGTGTTCCCTTTGGCTC
CTGGGTACAATACTGATATTGTGCTCAGTAGACAACCACGGTCTCAGGAGATGTCTGATTTC
CACAGACATGCACCATATAGAAGAGAGTTTCCAAGAAATCAAAGAGCCATCCAAGCTAAGG
ACACCTTCCCAAATGTCACTATCCTGTCCACATTGGAGACTCTGCAGATCATTAAGCCCTTA
GATGTGTGCTGCGTGACCAAGAACCTCCTGGCGTCTTACGTGGACAGGGTGTCAAGGATCA
TCAGGAGCCAAACCCAAAATCTTGAGAAAAATCAGCAGCATTGCCAACTCTTTCCTCTACA
TGCAGAAAATCTGCGGCAATGTGAGAACAGAGGCAGTGTCACTGCAGGCAGGAAGCCACC
AATGCCACCAGAGTCATCCATGACAACTATGATCAGCTGGAGGTCCACGCTGCTGCCATTAA
ATCCCTGGGAGAGCTCGACGTCTTTCTAGCCTGGATTAATAAGAATCATGAAGTAATGTTCT
CAGCTTGATGACAAGGAACCTGTATAGTGATCCAGGGATGAACACCCCTGTGCGGTTTACT
GTGGGAGACAGCCACCTTGAAGGGGAAGGAGATGGGGAAGGCCCTTGACAGCTGAAAGTCC
CACTGGCTGGCCTCAGGCTGTCTTATTCGCTTGAAATAGGCAAAAGTCTACTGTGGTAT
TTGTAATAAACTCTATCTGCTGAAAGGGCCTGCAGGCCATCCTGGGAGTAAAGGGCTGCCTT
CCCATCTAATTTATTGTAAAGTCATATAGTCCATGTCTGTGATGTGAGCCAAGTGATATCCT
GTAGTACACATTGTACTGAGTGGTTTTCTGAATAAATCCATATTTTACCTATGA

FIGURE 322

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA92282

><subunit 1 of 1, 177 aa, 1 stop

><MW: 20452, pI: 8.00, NX(S/T): 2

MKLQCVSLWLLGTILILCSVDNHGLRRCLISTDMHHIEESFQEIKRAIQAKDTFPNVTILST
LETLQIIKPLDVCCVTKNLLAFYVDRVFKDHQEPNPKILRKISSIANSFLYMQKTLRQCQEQ
RQCHCRQEATNATRVIHNDYDQLEVHAAAIKSLGELDVFLAWINKNHEVMFSA

Signal sequence:

amino acids 1-18

N-glycosylation sites.

amino acids 56-60, 135-139

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 102-106

N-myristoylation site.

amino acids 24-30

Actinin-type actin-binding domain signature 1.

amino acids 159-169

FIGURE 323

CCCGTGCCAAGAGTGACGTAAGTACCGCCTATAGAGTCTATAGGCCCACTTGGCTTCGTTAG
 AACGCGGCTACAATTAATACATAACCTTATGTATCATACACATACGATTTAGGTGACACTAT
 AGAATAACATCCACTTTGCCTTTCTCTCCACAGGTGTCCACTCCCAGGTCCAAGTGCACCTC
 GGTTCTATCGATAATCTCAGCACCAGCCACTCAGAGCAGGGCACGATGTTGGGGGCCCGCCT
 CAGGCTCTGGGTCTGTGCCTTGTGCAGCGTCTGCAGCATGAGCGTCCTCAGAGCCTATCCCA
 ATGCCTCCCCACTGCTCGGCTCCAGCTGGGGTGGCCTGATCCACCTGTACACAGCCACAGCC
 AGGAACAGCTACCACCTGCAGATCCACAAGAATGGCCATGTGGATGGCGCACCCCATCAGAC
 CATCTACAGTGCCCTGATGATCAGATCAGAGGATGCTGGCTTTGTGGTGATTACAGGTGTGA
 TGAGCAGAAGATACCTCTGCATGGATTTAGAGGCAACATTTTGGATCACACTATTTTCGAC
 CCGGAGAAGTGCAGGTTCACACACAGACGCTGGAACACGGGTACGACGTCTACCACTCTCC
 TCAGTATCACTTCTCTGGTCAGTCTGGGCCGGGCGAAGAGAGCCTTCCTGCCAGGCATGAACC
 CACCCCCGTACTCCAGTTCTCTGTCCCGGAGGAACGAGATCCCCCTAATTCACCTCAACACC
 CCCATACCACGGCGGCACACCCGGAGCGCCGAGGACGACTCGGAGCGGGACCCCCGTAACGT
 GCTGAAGCCCCGGGCCCGGATGACCCCGGCCCGGCTCCTGTTACAGGAGCTCCCGAGCG
 CCGAGGACAACAGCCCGATGGCCAGTGACCCATTAGGGGTGGTCAGGGGCGGTGAGTGAAC
 ACGCACGCTGGGGGAACGGGCCCGGAAGGCTGCCGCCCTTCGCCAAGTTCATCTAGGGTCTG
 CTGG

FIGURE 324

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142238

><subunit 1 of 1, 251 aa, 1 stop

><MW: 27954, pI: 9.22, NX(S/T): 1

MLGARLRLWVCALCSVCSMSVLRAYPNASPLLGSWGLIHLTYTATARNSYHLQIHKNQHV
GAPHQTIYSALMIRSEDAGFVVITGVMSRRYL CMDFRGNI FGSHYFDPENC RFQHQTLENGY
DVYHSPQYHFLVSLGRAKRAFLPGMNPPPYSQLSRNEIPLIHFNTPIPRRHTRS AEDDSE
RDPLNLVKPRARMT PAPASCSQELPSAEDNSPMASDPLGVVRGGRVNT HAGGTGPEGCRPFA
KFI

Important features of the protein:**Signal peptide:**

amino acids 1-24

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 175-179

N-myristoylation site.

amino acids 33-39, 100-106, 225-231, 229-235

HBGF/FGF family proteins

amino acids 73-124

FIGURE 325

GGAAAAGGTACCCGCGAGAGACAGCCAGCAGTTCTGTGGAGCAGCGGTGGCCGGCTAGG**ATG**
 GGCTGTCTCTGGGGTCTGGCTCTGCCCCCTTTCTTCTTCTGCTGGGAGGTTGGGGTCTCTGG
 GAGCTCTGCAGGCCCCAGCACCCGAGAGCAGACACTGCGATGACAAACGGACGACACAGAAG
 TGCCCGCTATGACTCTAGCACCCGGGCCAGCGCGCTCTGGAAACTCAAACGCTGAGCGCTGAG
 ACCTCTTCTAGGGCCTCAACCCAGCCGGCCCCATTCAGAAGCAGAGACCAGGGGAGCCAA
 GAGAATTTCCCTGCAAGAGAGACCAGGAGTTTCAAAAAACATCTCCAACTTATGTTGC
 TGATCGCCACCTCCGTGGAGACATCAGCCGCCAGTGGCAGCCCCGAGGGAGCTGGAATGACC
 ACAGTTACAGACCATCAGAGCAGTGATCCCGAGGAAGCCATCTTTGACACCTTTGACCCGA
 TGACAGCTCTGAAGAGGCAAAGACACTCACAATGGACATATTGACATTGGCTCACACCTCCA
 CAGAAGCTAAGGGCCTGTCTCTAGAGAGCAGTGCCTCTTCCGACGGCCCCCATCCAGTCATC
 ACCCCGTACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATACCCCC
 GTCACGGGCCTCAGAGAGCAGCGCCTCTTCCGACGGCCCCCATCCAGTCATACCCCCGTAT
 GGTCCCCGGGATCTGATGTCACTCTCCTCGCTGAAGCCCTGGTGACTGTCAAAACATCGAG
 GTTATTAATTGACAGCATCAGAAATAGAAACAACACTTCCAGCATCCCTGGGGCCTCAGA
 CATAGATCTCATCCCCACGGAAGGGGTGAAGGCCCTCGTCCACCTCCGATCCACCAGCTCTGC
 CTGACTCCACTGAAGCAAAACACACATCACTGAGGTACAGCCTCTGCCGAGACCCTGTCC
 ACAGCCGGCACCACAGAGTCAGCTGCACCTCATGCCACGGTTGGGACCCCACTCCCACTAA
 CAGCGCCACAGAAAGAGAAGTGACAGCACCCGGGGCCACGACCCCTCAGTGGAGCTTGGTCA
 CAGTTAGCAGGAATCCCTTGAAGAAACCTCAGCCCTCTCTGTTGAGACACCAAGTTACGTC
 AAAGTCTCAGGAGCAGCTCCGGTCTCCATAGAGGTGGGTGACAGTGGGCAAAACAACCTT
 CTTTGCTGGGAGCTCTGCTTCCTCCTACAGCCCTCGGAAGCCGCCCTCAAGAACTTACCC
 CTTACAGACACCGACCATGGACATCGCAACCAAGGGGCCCTTCCCCACGAGCAGGGACCTT
 CTTCTTCTGTCCCTCCGACTACAACCAACAGCAGCCGAGGGACGAACAGCACCTTAGCCAA
 GATCAAACTCAGCGAAGACCACGATGAAGCCCCAACAGCCACGCCACGACTGCCGGAC
 GAGGCCGACCACAGACG**TGA**GTGCAGGTGAAAATGGAGTTTCTCTCTCTGCGGTGAGTG
 TGGCTTCCCCGAAGACCTCACTGACCCAGAGTGGCAGAAAGGCTGATGCAGCAGCTCCAC
 CGGAACTCCACGCCACGCGCCTCACTTCCAGGTCTCCTTACTGCGTGTGAGGAGGCTA
 ACGGACATCAGCTGCAGCCAGGCATGTCCCGTATGCCAAAAGAGGGTGCTGCCCTAGCCTG
 GGCCCCACCGACAGACTGCAGCTGCGTTACTGTGCTGAGAGGTACCCAGAAGGTTCCCATG
 AAGGGCAGCATGTCCAAGCCCCAACCCAGATGTGGCAACAGGACCTCGCTCACATCCAC
 CGGAGTGTATGTATGGGAGGGGCTTCACTGTTCAGAGGTGTCTTGGACTCACCTGG
 CAGATGTTCTGTGTTTCACTAAGAGAGACCTGATACCCATCTGTGTGCTTCCATCTGCA
 TTAATAATCACTCAGTGTGGCCCCAAAAAAA

FIGURE 326

MGCLWGLALPLFFFCWEVGVSGSSAGPSTRADTAMTTDDTEVPAMTLPAGHAALETQTL
 ETSSRASTPAGPIPEAETRGAKRISPAETRSFTKTSNFMVLIATSVETSAAAGSPEGAGM
 TTVQITITGSDPEEAI FDTLCDDSS EEA KLTMDILT LAHTSTEAKGLSSESSASSDGPHV
 ITPSRASESSASSDGPHPVITPSRASESSASSDGPHPVITPSWSPGSDVTL LAEALVTVTNI
 EVINCSITEIETTSSIPGASDIDLIPTEGVKASSTSDPPALPDSTEAKPHITEVTASAETL
 STAGTTESAAPHATVGTPLPTNSATEREVTAPGATTL SGALVTVSRNPLEETSALSVETPSY
 VKVGAAPVSI EAGSAVGKTTSFAGSSASSYSPSEAALKNFTPSETPTMDIATKGPFPTSRD
 PLPSVPPTTNSRGTNSTLAKITTS AKTMTKFPQQRPRPLPGRGRPQT

N-glycosylation sites:

amino acids 252-256, 445-449, 451-455

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 84-90

Casein kinase II phosphorylation sites.

amino acids 37-41, 108-112, 131-135, 133-137, 148-152, 165-169,
 246-250, 254-258, 256-260, 269-273, 283-287, 333-337, 335-339,
 404-408, 414-418, 431-435

N-myristoylation sites.

amino acids 2-8, 19-25, 117-123, 121-127, 232-238, 278-284, 314-
 320, 349-355, 386-392, 397-403, 449-455

ATP/GTP-binding site motif A (P-loop).

amino acids 385-393

FIGURE 327

GCGGAGCATCCGCTGCGGTCTCGCCGAGACCCCGCGGGATTGCGCGGTCTTCCGCGGG
 GCGCGACAGAGCTGTCTCGCACCTGGATGGCAGCAGGGGCGCGGGGTCTCTCGACGCCA
 GAGAGAAATCTCATCTGTGCGAGCTTCTTAAAGCAAACCTAAGACCAGAGGGAGGATTAT
 CCTTGACCTTTGAAGACCAAACTAACTGAAATTTAAATGTTCTTCGGGGGAGAGGGGAG
 CTTGACTTACACTTTGGTAATAATTGCTTCCTGACACTAAGGCTGTCTGCTAGTCAGAATT
 GCCTCAAAAAGAGTCTAGAAGATGTTGTCATTGACATCCAGTCATCTCTTCTAAGGGAATC
 AGAGGCAATGAGCCCGTATATACCTCAACTCAAGAAGACTGCATTAATCTTGGCTGTTCAAC
 AAAAAACATATCAGGGGACAAAGCATGTAACCTGATGATCTTCGACACTCGAAAAACAGCTA
 GACAACCCAACTGCTACCTATTTTCTGTCCCAACGAGGAAGCCTGTCCATTGAAACCAGCA
 AAAGGACTTATGAGTTACAGGATAATTACAGATTTTCCATCTTTGACCAGAAATTTGCCAAG
 CCAAGAGTTACCCAGGAAGATTCTCTTACATGGCCAAATTTTCAACAGCAGTCACTCCCC
 TAGCCCATCATCACACAGATTATTCAAAGCCACCGATATCTCATGGAGAGACACACTTCT
 CAGAAGTTTGGATCCTCAGATCACCTGGAGAACTATTTAAGATGGATGAAGCAAGTGCCCA
 GCTCCTTGCTTATAAGGAAAAAGGCCATTCTCAGAGTTCACAAATTTTCTCTGATCAAGAAA
 TAGCTCATCTGCTGCCTGAAATGTGAGTGCGCTCCAGCTACGGTGGCAGTTGCTTCTCCA
 CATACCACCTCGGCTACTCCAAGCCCGCCACCTTCTACCCACCAATGCTTCAGTGACACC
 TTCTGGGACTTCCGACCCACAGCTGGCCACCACAGCTCCACCTGTAACCACTGTCACTTCTC
 AGCCTCCACGACCCCTATTTCTACAGTTTTTACAGCGGGCTCGGGCTACACTCCAAGCAATG
 GCTACAACAGCAGTTCTGACTACCACCTTTCAGGCACCTACGGACTCGAAAGGCAGCTTAGA
 AACCATACCGTTTACAGAAATCTCCAACCTTAACCTTTGAACACAGGGAATGTGTATAACCTA
 CTGCACTTTCTATGTCAAATGTGGAGTCTTCCACTATGAATAAACTGCTTCTCTGGGAAGGT
 AGGAGGGCCAGTCCAGGCAGTTCCTCCAGGGCAGTGTTCCAGAAATCAGTACGGCCTTCC
 ATTTGAAAAATGGCTTCTATCGGGTCCCTGCTCTTTGGTGCTCTGTTCTGGTGATAGGCC
 TCGTCTCTCTGGGTAGAATCCTTTCGGAATCACTCCGAGGAAACGTTACTCAAGACTGGAT
 TATTTGATCAATGGGATCTATGTGGACATCTAAGGATGGAATCGGTCTCTCTTAAATTCATT
 TAGTAACCAGAAGCCCAATGCAATGAGTTTCTGCTGACTTGCTAGTCTTAGCAGGAGGTG
 TATTTTGAAGACAGGAAAAATGCCCTTCTGCTTCTCTTTTTTTTTTGGAGACAGAGTCTT
 GCTCTGTTGCCAGGCTGGAGTGCAGTAGCACGATCTCGGCTCTCACCGAACCTCCGTCCTC
 CTGGGTTCAAGCGATTCTCTCGCTCAGCCTCCTAAGTATCTGGGATTACAGGCATGTGCCA
 CCACACTGGGTGATTTTGTATTTTAGTAGAGACGGGGTTTACCATTGTTGGTCAGGCTG
 GTCCTAAACTCCTGACCTAGTGATCCACCCTCTCGGCTCCCAAGTGCTGGGATTACAGG
 CATGAGCCACCACAGCTGGCCCTTCTGTTTTATGTTTGGTTTTTGGAGAGGATGAAGTG
 GGAACCAATTAGGTAATTTGGGTAATCTGTCTCTAAATATTAGCTAAAAACAAGCTCT
 ATGTAAAGTAATAAGTATAATTGCCATATAAATTTCAAATTTCAACTGGCTTTTATGCAAA
 GAAACAGGTTAGGACATCTAGGTTCCAATTCATTACATTTCTGGTTCCAGATAAAATCAAC
 TGTTTATATCAATTTCTAATGGATTTGCTTTCTTTTATATGGAATTCCTTTAAACTTATT
 CCAGATGTAGTTCCTCCAATTAATATTGTAATAAATCTTTTGTTACTCAA

FIGURE 328

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA45410
 ><subunit 1 of 1, 431 aa, 1 stop
 ><MW: 46810, pI: 6.45, NX(S/T): 6
 MFFGEGESLTYTLVIIICFLTLRLSASQNCLKKSLEDVVIDIQSSLSKGIRGNEPVYTSTQED
 CINSCCSTKNISGDKACNLMIFDTRKTARQPNCYLFFCPNEEACPLKPAKGLMSYRIITDFP
 SLTRNLPSQELPQEDSLLHGQFSQAVTPLAHHHTDYSKPTDISWRDTLSQKFGSSDHLEKLF
 KMDEASQQLLAYKEKGHSQSSQFSSDQEIAHLLPENVSALPATVAVASPHTTSATPKPATLL
 PTNASVTPSGTSQFQLATTAPPVTTVTTSQPPTTLISTVFTRAAATLQAMATTAVLTTFQAP
 TDSKGSLETIPFTEISNLTNTGNVYNPTALSMNSVESSTMNKTASWEGREASPGSSSQGSV
 PENQYGLPFEKWLIGSLLFGVFLVIGLVLLGRILSESRLRRKRSRLDYLINGIYVDI

Signal sequence.

amino acids 1-25

Transmembrane domain.

amino acids 384-405

N-glycosylation sites.

amino acids 72-76, 222-226, 251-255, 327-331, 352-356

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 415-419

Tyrosine kinase phosphorylation site.

amino acids 50-57

N-myristoylation sites.

amino acids 4-10, 48-54, 315-321

FIGURE 329

CTCCCACGGTGTCCAGCGCCCA**AATG**CGGCTTCTGGTCTGCTATGGGGTTGCGCTGCTGCT
 CCCAGGTTATGAAGCCCTGGAGGGGCCAGAGGAAATCAGCGGGTTCGAAGGGGACACTGTGT
 CCCTGCAGTGCACCTACAGGGAAGAGCTGAGGGACCACCGGAAGTACTGGTGCAGGAAGGTT
 GGGATCCTCTTCTCTCGTGTCTTGGCACCATCTATGCAGAAGAAGGCCAGGAGACAAT
 GAAGGGCAGGGTGTCCATCCGTGACAGCGCCAGGAGCTCTCGCTCATTGTGACCCTGTGGA
 ACCTCACCCTGCAAGACGCTGGGGAGTACTGGTGTGGGGTCGAAAAACGGGGCCCCGATGAG
 TCTTTACTGATCTCTCTGTTCGTCTTCCAGGACCTGCTGTCTCCCTCCCTTCTCCAC
 CTTCCAGCCTCTGGCTACAACAGCCTGCAGCCCAAGGCAAAAGCTCAGCAAAACCAGCCCC
 CAGGATTGACTTCTCTGGGCTCTACCCGGCAGCCACCACAGCCAAGCAGGGGAAGACAGGG
 GCTGAGGCCCTCCATTGCCAGGGACTTCCAGTACGGGCACGAAGGACTTCTCAGTAGAC
 AGGAACCTCTCCTCACCAGCGACCTCTCCTCCTGCAGGGAGCTCCCGCCCCCATGACAG
 TGGACTCCACCTCAGCAGAGGACACAGTCCAGCTCTCAGCAGTGGCAGCTCTAAGCCAGG
 GTGTCCATCCCGATGGTCCGCATACTGGCCCCAGTCTCTGGTGTGCTGAGCCTTCTGTACAG
 CGCAGGCCGTGATCGCCTTCTGCAGCCACTGCTCCTGTGGGGAAGGAAGCTCAACAGGCCA
 CGGAGACACAGAGGAACGAGAAGTTCTGGCTCTCAGCCTTACTGCGGAGAAAGGAAGCC
 CCTTCCCAAGCCCTGAGGGGGACGTGATCTCGATGCTCCTCCCTCCACACATCTGAGGAGGA
 GCTGGGCTTCTCGAAGTTTGCTCAGC**G**TAGGGCAGGAGGCCCTCCTGGCCAGGCCAGCAGT
 GAAGCAGTATGGCTGGCTGGATCAGCACCGGATTCCCGAAAGCTTTCACCTCAGCCTCAGAG
 TCCAGCTGCCCGACTCCAGGGCTCTCCCAACCTCCCGAGGCTCTCCTTTCGATGTTTCA
 GCCTGACCTAGAAGCGTTTGTACGCCCTGGAGCCAGAGCGGTGGCCTTGCTTCCCGCTG
 GAGACTGGGACATCCCTGATAGGTTACATCCCTGGGCAGAGTACCAGGCTGCTGACCCTCA
 GCAGGGCCAGACAAGGCTCAGTGGATCTGGTCTGAGTTTCAATCTGCCAGGAACCTCCTGGGC
 CTCATGCCCAGTGTGGACCTGCCTTCTCCCACTCCAGACCCACCTTGTCTTCCCTCCC
 TGGCTCCTCAGACTTAGTCCCACGGTCTCCTGCACTCAGCTGGTGATGAAGAGGAGCATGCT
 GGGGTGAGACTGGGATTCTGGCTTCTCTTTGAACACCTGCATCCAGCCCTTCAGGAAGCCT
 GTGAAAAACGTGATTCTTGGCCCCACCAAGACCCACAAAACCATCTCTGGGCTTGGTGACG
 GACTCTGAATTTCAACAATGCCCAGTGACTGTGCACTTGAGTTTGAAGGCCAGTGGGCTCG
 ATGAACGCTCACACCCCTTCAGCTTAGAGTGTGCATTGGGCTGTGAGCTCTCCACTGCC
 CAATAGATCTGCTCTGTCTGCGACACAGATCCACGTGGGACTCCCTGAGGCCCTGCTAAG
 TCCAGGCCCTTGGTCAGGTCAAGTGCACATTGCAGGATAAGCCAGGACCGGCACAGAAGTGG
 TTGCCCTTTNCCATTTGCCCTCCCTGGNCCATGCCTTCTTGCCTTTGGAAAAAATGATGAAGA
 AAACTTGGCTCCTTCTTGTCTGGAAGGGTTACTTGCTATGGGTTCTGGTGGCTAGAGA
 GAAAGTAGAAAAACAGAGTGCACGTAGGTGTCTAACACAGAGAGATAGAACAGGGCGG
 ATACCTGAAGGTGACTCCGAGTCCAGCCCCCTGGAGAAGGGGTGGGGGTGGGTGAAGTA
 GCACAACCTACTATTTTTTTCTTTTCCATTATTATTGTTTTTAAGACGAATCTCTGTGCT
 GCTGCCAGGCTGGAGTGCAAGTGGCAGCATCTGCAAACTCCGCTCTGGGTTCAAGTGATT
 CTTCTGCCTCAGCCTCCCGAGTAGCTGGGATTACAGGCACGCACCACCACCTGGCTAATT
 TTTGTACTTTTAGTAGAGATGGGGTTTACCATTGTTGGCCAGGCTGGTCTTGAACCTCTGAC
 CTCAAATGAGCCTCTGCTTCAGTCTCCCAAAATGCCGGGATTACAGGCATGAGCCACTGTG
 TCTGGCCCTATTTCCTTTAAAAAGTGAATTAAGAGTTGTTTCAGTATGCAAAACTTGGAAAG
 ATGGAGGAGAAAAAGAAAAAGGAAGAAAAAAATGTACCCATAGTCTCACCAGAGACTATCAT
 TATTTCTGTTTTGTTGTAATTCCTTCCACTCTTTTCTTCTTACATAAATTTGCCGGTGTCTTT
 TTTACAGAGCAATTATCTTGTATATACAACCTTGTATCTGCTTTTCCACCTTATCGTTCC
 ATCACTTTATTCAGCACTTCTGTGTTTTTACAGCCTTTTATAAATAAAATGTTTCATCA
 GCTGCATAAAAAAAAAAAAAA

FIGURE 330

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44196

<subunit 1 of 1, 332 aa, 1 stop

<MW: 36143, pI: 5.89, NX(S/T): 1

MRLLVLLWGCLLLPGYEALEGPPEETSGFEGDTVSLQCTYREELRDHRKYWCRKGGILFSRCS
GTIYAE EEGQETMKGRVSIRDSRQELSLIVTLWNLTLDAGEYWC GVEKRGPD ESSLISLFV
FPGPCCPPSPSPTFQPLATTRLQPKAKAQQTQPPGLTSPGLYPAATTAKQGKTGAEAPPLPG
TSQYGHERTSQYTGTSPHPATSPAGSSRPFMQLDSTSAEDTSPALSSGSSKPRVSIFMVRI
LAPVLVLLSLLSAAGLIAFCSHLLLWRKEAQQATETQRNEKFWLSRLTAE EKEAPSQAPEGD
VISMPPLHTSEELGFSKFVSA

Important features:**Signal peptide:**

amino acids 1-17

Transmembrane domain:

amino acids 248-269

N-glycosylation site.

amino acids 96-99

Fibrinogen beta and gamma chains C-terminal domain.

amino acids 104-113

Ig like V-type domain:

amino acids 13-128